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1, 2004, 17:21:01; Search time 10.2222 Seconds (without alignments) 84.690 Million cell updates/sec OM protein - protein search, using sw model March Run on:

US-09-905-083-33 40 1 LLLPLQILL 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADIES

	Description	serine proteinase	hypothetical profe		surfactant protein	conglutinin precur	conglutinin - bovi	mpeten	cation transport P	hypothetical prote		ď	hypothetical prote	뉟	_	hypothetical prote	O-antigen transpor	amyloid precursor-	T-cell surface gly	T-cell surface gly	-binding	(EC 3.4	9	hypothetical prote	1-acyl-sn-glycerol	probable acyltrans	tax-responsive ele	ge	stromelysin 3 (EC	_
SUMMARIES	ID	5396	H75201	3	833603		145878	AE0614	D97163	G65039	E70890	AB3334	C91063	AC0834	C83103	A90083	A69149	A46362	825656	RWHUT8	LNRTMA	KYHUCM	F91095	B85941	AC2620	C97402	C730	C485	ò	A44399
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Na+/H+-exchanging peptidyl-dipeptida apolipoprotein C-I	interleukin-2 prec conserved hypothet alpha-2u-globulin	hypothetical prote nitrate ABC transp probable secreted	hypothetical prote hypothetical prote probable permease	ABC transporter, m hypothetical prote hypothetical prote hypothetical prote
A12088 A31759 A38685	A31278 G75555 S10125	743766 F69260 T35589	T38931 C84914 A98157	AH3130 D83934 C84306 A71875
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30 31	1 W W W 1 W 4 W		1 W 4 4	44 44 44 ሪሳ የረ 44 ብኒ

#### ALIGNMENTS

J. Biol. Chem. 269, 19426-19426, 1994 A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzym A;Tetle: Cloning, expression, and characterization of stratum corneum chymotryptic enzym A;Gereace number: A53968; MUID:9430825; PMID:8034709 A;Status: preliminary A;Status: preliminary A;Coros: references: GB:133404; NID:9521214; PIDN:AAC37551.1; PID:9532504 A;Cross: references: GB:37730 A;Gene: GDB:PRSS6; SCCE A;Genetics: A;Gene: GDB:PRSS6; SCCE A;Genetics: A;Gene: GDB:77730 A;Map position: 7435-7435 C;Superfamily: trypsin; trypsin; homology F;30-245/Domain: trypsin; homology CRR> C;Superfamily: trypsin; trypsin; trypsin; homology CRR> C;Superfamily: homology CRR
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RESULT 2

Hypotherical protein PAB0088 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Accession: H75201
R;anonymous, Genoscope
submitted to the RME Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struct
A;Reference number: A75001
A;Accession: H75001
A;Accessi

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A; Introns: 67/1; 106/1; 142/1; 178/1; 217/1; 245/1
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                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-371 <SUZ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: JC2396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: S36879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        surfactant protein D - bovine
Cispecies: Bos primigenius taurus (cattle)
Cipate: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
CiAccession: 833603
R;Lim, B.L.; Lu, J.; Reid, K.B.M.
Immunology 78, 159-165, 1993
A;Title: Structural similarity between bovine conglutinin and bovine lung surfactant pro
A;Reference number: 833603; MUID:93170856; PMID:8436402
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Cidte: 02-Feb-2001 #sequence_revision ...
Cidcession: H84314
R/M ...
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JN0450
conglutinin precursor - bovine
conglutinin precursor - bovine
NyAlternate names: C3D-binding protein
NyContains: conglutinin-N
C5ppedies: Bos primigenius taurus (cattle)
C5pates: 10-Sep-1999 #requence revision 10-Sep-1999 #text_change 16-Jun-2000
C5pate: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 16-Jun-2000
C5.Accession: JN0450; JC2396; $33235; A23740; S36879; S35644; I46010; A29416; S34054
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A;Accession: H84314
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-277 <STO>
A;Residues: GB:AE004437; NID:g10581096; PIDN:AAG19884.1; GSPDB:GN00138
A;Genetics:
A;Gene: ccp
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                                                                                                                                                                                                                                                                                                                                                                                         cytochrome aa3 controlling protein [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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C,Superfamily: pulmonary surfactant protein D; C-type lectin homology
F;248-367/Domain: C-type lectin homology <LCH>
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   Length 146;
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Pred. No. 41;
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Score 36; DB 2
Pred. No. 6.5;
2; Mismatches
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Pred. No. 31;
3; Mismatches
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Best Local Similarity 66.7
Matches 6; Conservative
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                                      Similarity 77.8
7; Conservative
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Best Local Similarity
Matches 7; Conserv
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       Query Match
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Matches 7
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Cross-references: EMBL:U06860; NID:9507183; PIDN:AAB60624.1; PID:9514256; Comment: This protein mediates the agglutination of erythrocytes with antibody and commiconment: This protein is a Ca2+-dependent serum lectin specific for N-acetylglucosamine;
                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: DDBJ: D14085; NID:9285643; PIDN:BAA03170.1; PID:9285644
A; Experimental source: liver
R; Experimental source: liver
R; Kawasaki, N.; Itoh, N.; Kawasaki, T.
B; Chen, Biophys. Res. Commun. 198, 59.-604, 1994
A; Title: Gene organization and 5' flanking region sequence of conglutinin: A C-type mamm?
A; Reference number: JC2396; WUID:94128104; PMID:8297370
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A;Residues: 1-371 <KA2>
A;Residues: 1-371 <KA2>
A;Note: The authors translated the codon GAT for residues 250 and 270 as Glu
R;Lu, J; Lauteen, S.B.; Thiel, S.; Jensenius, J.C.; Reid, K.B.M.
Biochem. J. 292, 157-162, 1993
A;Title: The cDNA cloning of conglutinin and identification of liver as a primary site
A;Reference number: S332355; MUID:93277452; PMID:7684896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rice, Y.M.; Leiby, K.R.; Allar, U.; Paris, K.; Lerch, B.; Okarma, T.B.
U. Biol. Chem. 266, 2715-2723, 1991
A;Title: Primary structure of bovine conglutinin, a member of the C-type animal lectin A;A;Reference number: A22740; WUID:91131556; PMID:1993651
A;Accession: A23740
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A;Title: Bovine conglutinin gene exon structure reveals its evolutionary relationship A;Reference number: 146010; MUID:94267222; PMID:8207234
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A,Residues: 21-5475-86, X', 88-89, X', 91, X', 93-94;208-209, X', 211-227 <KAW>
A,Residues: 21-5475-86, X', 88-89, X', 91, X', 93-94;208-209, X', 211-227 <KAW>
A,Residues: 21-5475-86, X', B.M.

Ext. J. Wiedemann, H.; Holmskov, U.; Thiel, S.; Timpl, R.; Reid, K.B.M.

Eur. J. Biochem. 215, 793-799, 1993
A,Title: Structural similarity between lung surfactant protein D and conglutinin. A,Reference number: S35044; WUID: 93358905; PMID: 8354286
A,Accession: 835044
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A;Mosidues 75-86,7%',88-89,7%',91,'I' <LUA>
A;Residues 75-86,7%',88-89,0%',91,'I' <LUA>
A;Experimental source: lung
R;Young, N.M., Leon, M.A.
B;Ochem. Blochyw. Bos. Commun. 143, 645-651, 1987
A;Title: The carbohydrate specificity of conglutinin and its homology to proteins
A;Reference number: A29416, MUID:87184551; PMID:3566740
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R; Malhotra, R.; Laursen, S.B.; Willis, A.C.; Sim, R.B.
Biochem. J. 293, 15-19, 1993
A; Title: Research Communication. Localization of the receptor-binding site in the A; Reference number: S34054; MUID:93319501; PMID:8328957
A; Contents: annotation
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A;Residues: 1-172,'H',174-217,'A',219-271,'V',273-371 <LUJ>
A;Cross-references: EMBL:X71774; NID:g395267; PIDN:CAA50665.1; PID:g395268
Krbuzuki, Y.; Yin, Y.P.; Makino, M.; Kurimura, T.; Wakamiya, N. Biochem. Biophys. Res. Commun. 191, 335-342, 1993
A;Title: Cloning and sequencing of a cDNA coding for bovine conglutinin. A;Reference number: JN0450; MUID:93213261; PMID:8460993
A;Mocession: JN0450
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A,Residues: 21-209, 'S', 211-371 <LEE>
R,Kawasaki, N.; Yokota, Y.; Kawasaki, T.
Arch. Blochem. Blophys. 305, 533-540, 1993
A,Tille: Differentiation of conglutination activity and
A,Tille: Differentiation of A,Reference number: S36879; MUID:93384312; PMID:8373191
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A;Molecule type: DNA
A;Residues: 1-371 <LIO>
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Cippecies: Escherichia coli
Cipate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
Cipate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
Cipate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
Riplattner. P. Ri. Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
Science 277, 1453-1462, 1997
A. Reference number: A64720, MulD:97426617; PMID:9278503
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70890
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Conior, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                              Cition transport P-type ATPase CAC2137 [imported] - Clostridium acetobutylicum Cispecies: Clostridium acetobutylicum Cispecies: Clostridium acetobutylicum Cispecies: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: D97163 G.; Gmelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, R;Nolling, J.; Bernett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Attle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D97163
A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: GB;AE001437; PIDN:AAK80095.1; PID:g15025128; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum AICC824
C;Genetics:
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Pred. No. 97;
1; Mismatches 0; Indels
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82.5%; Score 33; DB 2; Length 196;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 1; Indels
        Indels
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        1; Mismatches
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Best Local Similarity 87.5-
                 7; Conservative
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E70890
                      Matches
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5.Species: Salmonella enterica subsp. enterica serovar Typhi
A.Note: this species has also been called Salmonella typhi
C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 25-Aug-2003
C.Accession: AE0614
R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, F.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, S.; Connetton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A.; Muthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serow A; Reference number: AB0502; MUID:21534947; PMID:11677608
    C; Superfamily: pulmonary surfactant protein D; C-type lectin homology
C; Keywords: calcium binding; glycoprotein; hydroxylysine; hydroxyproline
F; 1-20/Domain: signal sequence #status predicted <SiG>F; 1-20/Domain: signal sequence #status predicted <MAT>
F; 21-371/Product: conglutinin #status predicted <MAT>
F; 46-214/Region: collagen-like
F; 55-371/Product: conglutinin-N #status predicted <MAZ>
F; 52-371/Product: conglutinin-N #status predicted <MAZ>
F; 53-371/Product: conglutinin-N #status predicted <MAZ>
F; 53-37, 99, 135, 141, 159, 162, 198, 210/Modified site: 5-hydroxylysine (Lys) #status experime
F; 78, 96, 108, 111, 129, 132, 147, 153, 171, 195/Modified site: 5-hydroxyproline (Pro) #status experime
F; 78, 99, 132, 114, 159, 162, 198, 171, 195/Modified site: 4-hydroxyproline (Pro) #status experimental
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Cipate: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 20-Aug-1999
Cipate: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 20-Aug-1999
Cipate: 145879 #sequence_revision 19-Dec-1997 #text_change 20-Aug-1999
Cipate: 145879 #sequence_revision 18-Dec-1997 #text_change 20-Aug-1999
Ridou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry
Gene 141, 277-281, 1994
A.Title: Bovine conglutinin (BC) mRNA expressed in liver: cloning and characterization capacers on number: 145878
A.Accession: 145878
A.A
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A,Molecule type: DNA
A,Residues: 1-754 <PAR>
A,Cross_references: GB:AL513382; PIDN:CAD05383.1; PID:g16502146; GSPDB:GN00176
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Pred. No. 42;
1; Mismatches 1; Indels
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85.0%; Score 34; DB 2; Length 371;
Best Local Similarity 77.8%; Pred. No. 42;
Matches 7; Conservative 1; Mismatches 1; Indels
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86;
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Pred. No.
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Best Local Similarity 77.8%;
Matches 7; Conservative
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LLLPLSVLL 10
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77.8%; Pred. No. 71; ive 1; Mismatches
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                                                7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity
7, Conserva
        Best Local Similarity
Matches 7; Conserv
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A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70890
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-282 <COL>
A;Cross-references: GB:AL022073; GB:AL123456; NID:93256024; PIDN:CAA17851.1; FID:e125651
A;Genetics:
A;Genetics:
A;Genetics:
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Cibate: 0.1 Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
Cibate: 0.0 Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
Cibaccesion: AB3334
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, B.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443.448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Status: preliminary
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daunorubicin resistance transmembrane protein [imported] - Brucella melitensis (strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.5%; Score 33;
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C;Superfamily: hypothetical protein H10107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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probable membrane protein corB [imported] - Salmonella enterica subsp. enterica serovar 7 () Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Davecies has also been called Salmonella typhi C;Davecies has also been called Salmonella typhi C;Davecies Heatled Salmonella typhi C;Davecies has also been called Salmonella typhi C;Davecies has also been called Salmonella typhi C;Davecies harving Li, Jouagan, G.;James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connetton, P.; Cronin, A.; Davies, R.M.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; OʻGacra, P.
Ayauthors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A; Reference number: ABOSO2; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathog A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G3103
A;Astus: preliminary
A;Molecule: preliminary
A;Molecule: Ltype: DNA
A;Molecule: 1-426 <6770>
A;Residues: 1-426 <6770>
A;Accessives: 08:AE004850; GB:AE004091; NID:g9950560; PIDN:AAG07726.1; GSPDB:GN001: A;Genetics: A;Genetics
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C.Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C.Accession: C33103
R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br.
R.Stover, C.Y.; Y. Brody, L.L.; Coulter, S.N.; Polger, K.R.; Kas, A.; Larbig, K.; Lim,
I.Lory, S.; Olson, M.V.
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A)Status: preliminary
A)Molecule type: DNA
A)Molecule type: DNA
A)Regidues: 1-413 <PAR>
A)CROSSES references: GB:AL513382; PIDN:CAD05858.1; PID:gl6503833; GSPDB:GN00176
C)Genetics:
A)Genetics:
A)Genetics:
C)Superfamily: hypothetical protein H10107
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A90083
hypothetical protein orf470 [imported] - Guillardia theta nucleomorph
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Pred. No. 73;
1; Mismatches 1; Indels
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C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Dates: 0. 34-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: A90083
R;Douglas, S; Zauner, S; Fraunholz, M.; Beaton, M.; Penny, S; Deng, L.T.; Wu, X.; Rei
R;Douglas, S; Zauner, S; Fraunholz, M.; Beaton, M.; Penny, S; Deng, L.T.; Wu, X.; Rei
R;Douglas, S; Zauner, S; Fraunholz, M.; Beaton, M.; Penny, S; Deng, L.T.; Wu, X.; Rei
A;Reference number: A90082; MUID:11323671; PMID:11323671
A;Reference number: A90083
A;Retus: preliminary
A;Molecule type: DNA
A;Residues: 1-470 < DOU>A;Residues: 1-470 < DOU>A;Generics:
A;Generics:
A;Gene
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Best Local Similarity 66.7%; Pred. No. 84;
Matches 6; Conservative 3; Mismatches 0; Indels
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253 MLLPLEILI 261
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Search completed: March 1, 2004, 17:36:28 Job time: 12.3333 secs

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P49862 homo sapien 0941m7 mus musculu 077755 trichosurus p35246 bos taurus 28365 bos taurus p23805 bos taurus p23806 bos taurus p37908 escherichia 660813 homo sapien 060810 homo sapien p19999 rattus musculu p30433 pongo pygma p01732 homo sapien p56435 macaca fasc p52195 papico hamad 002853 mus musculu p12821 homo sapien p23916 cavia porce 077501 cavia porce 07760 cavia porce p1708 rattus norv
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streptomyce
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mus musculu
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arabidopsis
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                                                                                      March 1, 2004, 17:17:25; Search time 6 Seconds (without alignments) 78:105 Million cell updates/sec
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Q13183
Q35305
Q70174
P09483
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P87052
Q02818
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Q9bvt8
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                                                                                                                                                                                                                                                                                        141681
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                         141681 seqs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
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EL46 BOVIN
CONG BOVIN
YATO ECOLI
YATO ECOLI
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COBA HUMAN
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Z CAVPO
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YDJ4_SCHPO
NCB1_HUMAN
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Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 LLLPLQILL 9
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Match Length DB
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Perfect score:
                                                                                                                                                                                                                Scoring table:
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                                                                                                                                                                                       Sequence:
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No.
                                                                                              Run on:
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P51693 homo sapien P4946 mus musculu P23469 homo sapien Q94666 mus musculu Q97514 homo sapien P97798 mus musculu Q96790 homo sapien P98161 homo sapien P43030 sus sazien P43030 sus sazien P26994 pseudomonas P26991 sus sazien P26991 sus sazien
APP1 HUMAN PTPE_MOUSE PTPE_HOWSE U84A MOUSE CHC2 HUMAN NEO1_MOUSE PKD1 HUMAN SZO7_FIG EXSB_PEGE IL2_PIG IL2_PIG
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6550 6650 7000 110004 83298 1119 1119 1154
777.58 777.75 777.75 77.75 77.75 77.75 77.75 77.75 77.75 77.75

#### ALIGNMENTS

KLEYLT 1 KLK7 HUMAN  TO ACL PA9862;  AC PA9862;  AC PA9862;  AC PA9862;  AC PA9862;  AC LOCT-1996 (Rel. 34, Created)  DT 01-0CT-1996 (Rel. 34, Last sequence update)  DT 10-0CT-2003 (Rel. 42, Last annotation update)  DE Kallikrein 7 precursor (EC 3.4.21) (Stratum corneum chymotryptic corrupts)  KLK7 OR PRSS6 OR SCCE.  GN KLK7 OR PRSS6 OR SCCE.  GN CACE.  C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  C Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.  NCB1 Tax1D=9606;	SEQUE SEQUE TISSI TISSI MEDL: REDEL: Cloi Chymc	-00 - 20 2 m - m 20 2 - 00 -	-0 x x = e 0 - 0 x 0 = 0 = 1
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cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines.

TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Very low levels are also seen in the brain and kidney.

SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KALLIKREIN 7.
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PROSTIE; PS502134; TRYPSIN, DOM; 1.
PROSTIE; PS00135; TRYPSIN, BIS; 1.
PROSTIE; PS00135; TRYPSIN, BIS; 1.
Hydrolase; Serine procease; Zymogen; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 604438; -
GO: 60:0008236; F:serine-type peptidase activity; TAS.
GO: 60:0008245; P:epidermal differentiation; TAS.
InterPro; IPR009003; Cys. Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATION PEPTIDE.
                                                                                                                                                                                                                                                                                              EMBL, L33404; AAC37551.1; -.
EMBL, AF166330; AAD49718.1; -.
EMBL, AF243527; AAG33360.1; -.
EMBL, AF332583; AAK69624.1; -.
PIK, A53968; A53968.
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                                                                                                                                                                                                                                                                                                                                                                                                             MERCPS; S01.300; -. Genew; HGNC:6368; KLK7.
MIM; 604438; -.
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DISULFID
CARBOHYD
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PROPEP
CHAIN
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0; Gaps
100.0%; Score 40; DB 1; Length 253; 100.0%; Pred. No. 0.97; ative 0; Mismatches 0; Indels
                  Best Local Similarity 100, Matches 9; Conservative
                                                                                     1 LILPLOILL 9
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Query Match

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FKII_MOUSE STANDARD; PRT; 201 AA.
Q9DIM7; Q9CRE4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
FKS06 binding protein 11 precursor (EC 5.2.1.8) (Peptidyl-prolyl cistrans isomerase) (Pplase) (Rotamase) (19 kDa FKS06-binding protein)
                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                    FKBP11.
                 FKII MOUSE

ID FKII M

PKII M

PKII M

PKII M

DT 28-FEB

DT 28-FEB

DE FKSO6

DE FKSO6

DE TANS

GN FKBPI
RESULT 2
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(omega=0).

In SIMILARITY: Belongs to the FKBP-type PPlase family.

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                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RAWAI T., SAIDE=EMBLYO;

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAWAI J., Saito J., Shinagawa H., Kondo S., Yamanaka I.,

A Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Ashburner M., Batalov S., Casavant T.,

Radora K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo T., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Flutuno M., Anno H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Rustincich S., Hill D., Hofmann M., Huwe D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Lyons P., Rato K., Schoenbach C., Seya T., Shibata Y., Storck K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATESCENDING, TISSUE-Mammary gland,

WEDLINE=2238827; PubMed=12477932,

REDLINE=2238827; PubMed=12477932,

REDLINE=2238827; PubMed=12477932,

RIAUBRE R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RIAUBRE R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

Blackelton M., Scares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E.,

Repleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Roberton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Roberton M., McKernan K.J., Marker J.A., Gunaratne P.H.,

Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Scherman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein synthesis.
-!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AKO0331; BAB22719.1; -.
EMBL; AKO19132; BAB31559.1; -.
EMBL; BC037596; AAH37596.1; -.
HSMP; BC0771; IFKJ.
MGD; MGI:1913370; FKbpl1.
Interpro; IPRO1179; FKBP_PPIASE.
PFAM; PF00254; FKBP; 1.
PROSITE; PS00453; FKBP_PPIASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                          NCBI_TaxID=10090;
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PSPD_BOVIN
P35246;
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PSPD_BOVIN
        SO THE FEFFFFF SO THE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=99027340; Pubmed=9801457;

AGREENE=99027340; Pubmed=9801457;

AGREENE=99027340; Pubmed=9801457;

Greenwood P.J., McNatty K.;

I.J. 111-152(1998).

J. Mol. Endocrinol. 211-141-152(1998).

J. Mol. Engolution. McTuraniol. 211-141-152(1998).

J. Mol. Engolution. 211-141-152(1998).

J. Mol. E
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
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                                                                                                           POTENTIAL.
FKSOG BINDING PROTEIN 11.
FRSOG BINDING PROTEIN 11.
S -> F (IN REF. 1; BAB31559).
S -> R (IN REF. 1; BAB31559).
S -> R (IN REF. 1; BAB31559).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS. INHIBIN A IS A DIMER OF ALPHA AND BETA-A. INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
-!- SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                              Match 95.0%; Score 38; DB 1; Length 201; Local Similarity 88.9%; Pred. No. 1.9; es 8; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF033340; AAC63945.1; -. GO, GO: 00005576; C:extracellular; ISS. GO, GO: 0005576; C:extracellular; ISS. GO; GO: 0001515; F:extrivin inhibitor activity; ISS. GO; GO: 00005125; F:extrivin activity; ISS. GO; GO: 00003793; F:Gefense/immunity protein activity; ISS. GO; GO: 00005179; F:bormone activity; ISS. GO; GO: 0005179; F:protein binding; ISS. GO; GO: 0005515; F:protein binding; ISS. GO; GO: 00005150; F:eroteil cycle arrest; ISS. GO; GO: 0001544; P:cell cycle arrest; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Inhibin alpha chain precursor.
PROSITE; PS00454; FKBP_PPIASE_2; FALSE_NEG.
PROSITE; PS50059; FKBP_PPIASE_3; 1.
Isomerase; Rotamase; Signal.
1.27 SIGNAL.
                                                                                                                                                                                                                                                                                                            22137 MW;
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                                                                                                                                                    201
144
53
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198
201 AA;
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077755;
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                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                               SIGNAL
                                                                                                                                                        CHAIN
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Matches
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IHH TRIVU

ITH TRIVU

DT 15-JU

DT 15-JU

DT 15-JU

DE 115-JU

DE 1
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GO; GO:0008151; P:cell growth and/or maintenance; ISS.

GO; GO:007166; P:cell surface receptor linked signal transdu. .; ISS.

BR GO; GO:0007267; P:cell-cell signaling; ISS.

BR GO; GO:000267; P:cell-cell signaling; ISS.

BR GO; GO:000551; P:hemoglobin biosynthesis; ISS.

BR GO; GO:000551; P:hemoglobin biosynthesis; ISS.

BR GO; GO:0045786; P:negative regulation of B-cell differentiation; ISS.

BR GO; GO:0045786; P:negative regulation of follicle-etimulating .; ISS.

BR GO; GO:0045879; P:negative regulation of follicle-etimulating .; ISS.

BR GO; GO:0045079; P:negative regulation of follicle-etimulating .; ISS.

BR GO; GO:0045079; P:negative regulation of follicle-etimulating .; ISS.

BR GO; GO:0045079; P:negative regulation of follicle-etimulating .; ISS.

BR GO; GO:0045079; P:negative regulation of follicle-etimulating .; ISS.

BR GO; GO:0045079; P:negative regulation of follicle-etimulating .; ISS.

BR GO; GO:0045079; P:negative regulation of follicle-etimulating .; ISS.

BR GO; GO:0045079; P:negative regulation of follicle-etimulating .; ISS.

BR GO; GO:0045079; P:negative regulation of follicle-etimulating .; ISS.

BR GO; GO:0045079; P:negative regulation of follicle-etimulating .; ISS.

BR GO; GO:0045079; P:negative regulation of follicle-etimulating .; ISS.

BR FAMILY PRODOGS; TGFED: 1.

BR RENING; PRODOGS; TGFED: 1.

BR SMRRI; SMOOO4; TGFE: 1.

BR SMRRI; SMOOO4; TGFE: 1.

BR SMRRI; SMOOO4; TGFE: 1.

BR SMRRI; PRODES .

BR SMRRI; PRODOGS .

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-!- FUNCTION: Contributes to the lung's defense against inhaled microorganisms. Binds strongly maltose residues and to a lesser extent other alpha-glucosyl moieties. It could participate in the extracellular reorganization or turnover of pulmonary surfactant.
-!- SUBSUNIT: Oligomeric complex of 4 set of homotrimers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FED-1999 (Rel. 39, Last annotation update)
Pulmonary surfactant-associated protein D precursor (SP-D) (FSP-D).
SFTPD OR SFTP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Bukanyota, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,

Bovidae, Bovinee, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB-Lung;
MEDLINE-93170856; PubMed-8436402;
Lim B.L., Lu J., Reid K.B.M.;
"Structural similarity between bovine conglutinin and bovine lung surfactant protein.D and demonstration of liver as a site of synthesis of conglutinin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 208-247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 266 N
361 AA; 38945 MW;
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Best Local Similarity 88.9
Matches 8; Conservative
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CONG BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
-!- MISCELLANEOUS: Pulmonary surfactant consists of 90% lipid and 10% protein. There are 4 surfactant-associated protein: 2 collagenous, carbohydrate-binding glycoproteins (SP-A and SP-D) and 2 small hydrophobic proteins (SP-B and SP-C).
-!- SIMILARITY: Contains 1 collagenous domain.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P35247; 1B08.
InterPro; IPR008160; Collagen.
InterPro; IPR008160; Lectin_C.
Pfam; PF01391; Collagen; 2.
Pfam; PF001391; Collagen; 2.
Pfam; PF00059; lectin c; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00610; C_TYPE_LECTIN_2; 1.
PROSITE; PS00610; C_TYPE_LECTIN_3; 0.
PROSITE; PS00610; PS00610; 0.
PROSITE; PS00610; 0.
PROSITE; PS00610; PS00610; 0.
PROSITE; PS00610; 0.
PROSIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PULMONARY SURFACTANT-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Ammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLLAGEN-LIKE.
COLLED COIL (POTENTIAL).
C-TYPE LECTIN (SHORT FORM).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ) (POTENTIAL).
HYDROXYLATION (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   liver.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Collectin-46 precursor (CL-46) (46 kDa collectin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 371 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X75911; CAA53510.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 77.6 tes 7, Conservative
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C146 BOVIN
C1246 BOVIN
DT 28-FEB-
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Lu J., Laursen S.B., Thiel S., Jensenius J.C., Reid B.M.;
"The cDNA cloning of conglutinin and identification of liver as a
primary site of synthesis of conglutinin in members of the Bovidae.";
Blochem. J. 292:157-162(1993).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93213261; PubMed=8460993; Suzuki Y., Yin Y., Makino M., Kurimura T., Wakamiya N.; Carining and sequencing of a cDNA coding for bovine conglutinin."; Biochem. Biophy9. Res. Commun. 191:335-342(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF509589; AAM34742.1; -
EMBL; AF509589; AAM34742.1; -
EMBL; AF509590; AAM34743.1; -
EMBL; AF509590; AAM34743.1; -
EMBL; AF509590; AAM34743.1; -
EMBL; PF001304; Lectin C; 1
PROSTE; PRO0619; CTYPE LECTIN 1; 1
PROSTE; PRO0619; CTYPE LECTIN 2; 1
Lectin; Hydroxylation; Glycoprotein; Mannose-binding; Membrane; Collagen; Repeat; Calcium; Signal...
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COLLAGEN-LIKE.
C-TYPE LECTIN (SHORT FORM).
CELL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                               similarity).
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Highly expressed in thymus and liver.
--- PIM: Hydroxylated (Potential).
--- PIM: Hydroxylated (Potential).
--- SIMILARITY: Contains 1 collagenous domain.
--- SIMILARITY: Contains 1 C-type lectin family domain.
SUBUNIT: Oligomeric complex of 4 set of homotrimers (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.0%; Score 34; DB 1; Length 371; 77.8%; Pred. No. 22;
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01.NOV-1991 (Rel. 20, Created)
01-PEB-1994 (Rel. 28, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
Conglutinin precursor.
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Best Local Similarity 77.8
Matches 7; Conservative
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WEDLINE-87184551; PubMed=3566740;

WEDLINE-87184551; PubMed=3566740;

Young N.W., Leon M.A.,

The carbohydrate specificity of conglutinin and its homology to

Proteins in the hepatic lectin family.";

Blochem. Blochys. Res. Commun. 143:645-651(1987).

Blochem. Blochys. Res. Commun. 143:645-651(1987).

Leoniplement component (CSD1). It is capable of binding nonreducing terminal Nacetylglucosamine, mannose, and fucese residues.

Complement component (CSD1). It is capable of binding nonreducing terminal Nacetylglucosamine, mannose, and fucese residues.

Complement component (CSD1). It is capable of binding nonreducing terminal Nacetylglucosamine, mannose, and fucese residues.

Complement of set of homotrimers.

Collagenous domain.

Colla
                                            TISSUE-Liver;
MEDLINE-94215917; PubMed=8163202;
Liou L.S., Sastry K., Hartshorn K.L., Lee Y.M., Okarma T.B.,
Tauber A.I., Sastry K.N.;
"Bovine conglutinin (BC) mRNA expressed in liver: cloning and
characterization of the BC cDNA reveals strong homology to surfactant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94128104; PubMed=8297370;
Kawasaki N., Itoh N., Kawasaki T.;
"Gene organization and 5'-flanking region sequence of conglutinin: a
C-type mammalian lectin containing a collagen-like domain.";
Biochem. Biophys. Res. Commun. 198:597-604(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 21-371.
MEDLINE=91131556; PubMed=1993651;
Lee Y.-M., Leiby K.R., Allar J., Paris K., Lerch B., Okarma T.B.;
"Primary structure of bovine conglutinin, a member of the C-type animal lectin family.";
J. Biol. Chem. 266:2715-2723(1991).
                                                                                                                                                                                                                                                                                                          MEDINE=94267222; PubMed=8207234;
Liou L.S., Sastry R., Hartshorn K.L., Lee Y.M., Okarma T.B.,
Tauber A.I., Sastry K.N.;
"Bovine conglutinin gene exon structure reveals its evolutionary
relationship to surfactant protein-D.";
J. Immunol. 153:173-180(1994).
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EMBL, X7174, CAA50665.1, -...
EMBL, U06860, AAB60624.1, -...
EMBL, U06854, AAB60624.1, -...
EMBL, U06854, AAB60624.1, JOINED.
EMBL, U06856, AAB60624.1, JOINED.
EMBL, U06856, AAB60624.1, JOINED.
EMBL, U06857, AAB60624.1, JOINED.
EMBL, U06859, AAB60624.1, JOINED.
EMBL, U06859, AAB60624.1, JOINED.
EMBL, U06859, AAB60624.1, JOINED.
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                                                                                                                                                                                                                    Gene 141:277-281(1994).
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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D25299; 1
D25300;
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STRAIN=K12 / MG1655.
STRAIN=K12 / MG1655.
Blatiner F.R., Pubmed=9278503;
Blatiner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                R PIR, 145878; 145878.

R PIR, 170450; JN0450.

R HESP: D3247; 1908.

R HESP: D3247; 1908.

R InterPro; 17800161; Clg helix.

R InterPro; 17800160; Collagen.

R InterPro; 178001304; Lectin.C.

R Prom, PF00059; lectin.C.

R Prom, PF000034; CLECT; 1.

R PROSITE; PS00014; CLECT; 1.

R PROSITE; PS00015; CTYPE LECTIN.1; 1.

R PROSITE; PS00011; CTYPE LECTIN.1; 1.

R PROSITE; PS00011; CTYPE LECTIN.2; 1.

R PROSITE; PS00011; CTYPE LECTIN.1; 1.

R PROSITE; PS00011; CTYPE LECTIN.2; 1.

R COllagen; Repeat; Calcium; Signal.
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HYDROXYLATION.

CELL ATTACHMENT SITE (POTENTIAL).

BY SIMILARITY.

N-LINKED (GLCNAC. . ) (POTENTIAL).

R -> H (IN REF. 2 AND 3).

K -> S (IN REF. 5).

V -> A (IN REF. 2).

E -> V (IN REF. 2).

W -> B (IN REF. 2).
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Pred. No. 22;
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C-TYPE LECTIN (SHORT FORM)
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MEDLINE=97349980; PubMed=9205837;
EMBL; D25301; BAA04983.2; JOINED
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NCBI_TaxID=562;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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|LLLPLSVLL 10
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272
371 AA;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed, Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL022101; CAA17880.1; -.
EMBL; AL049680; CAB41252.1; -.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.5%; Score 33; DB 1, Length 435; 87.5%; Pred. No. 40; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhodes S.;
submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the MAPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grafham D.; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                       Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                       Rhodes 5 ;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: Belongs to the MAPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435 AA; 50539 MW; 3D19443032BBB494 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypochetical protein D/845024.2 (Fragment).
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypotherical protein DJ845024.5 (Fragment)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         500 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 82.5
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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NON_TER 435 43
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                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                              NCBI_TaxID=9606;
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ID YA04 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AT THE PROPERTY AND A COURT OF THE PROPERTY AND A COURT OF
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Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takahashi H., Takeda J., Takemoto K., Ushara K., Wada C., Yamagata S., Horiuchi T.; "Construction of a contiguous 874-kb sequence of the Escherichia coli "Construction of a contiguous 874-kb sequence of the Escherichia coli analysis of its sequence features.";

DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=B178;
MEDLINE=88319942; PubMed=3045760;
Liphinska B., King J., Ang D., Georgopoulos C.;
"Sequence analysis and transcriptional regulation of the Escherichia coli grpE gene, encoding a heat shock protein.";
Nucleic Acids Res. 16:7545-7562(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 2 CBS domains.
-!- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 199 THAT PRODUCES TWO ORFS.
-!- CAUTION: Ref.3 sequence differs from that shown due to numerous frameshifts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION.

Rudd K.E.;

Unpublished observations (AUG-1994).

-!- SUBCELLULIAR LOCATION: Integral membrane protein (Potential).

-!- SIMILARIY: BELONGS TO THE UPF0053 FAMILY. STRONG, TO

H.INFLUENZAE HI0107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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EMBL; AE000347; AAC75661.1; ALT FRAME.
EMBL; D90888; BAA16497.1; ALT INIT.
EMBL; X07883; -1 NOT ANNOTATED_CDS.
EMGLS, X07831-1; NOT ANNOTATED_CDS.
ECGGene; EG12442; yfjb.
InterPro; IPR00545; CBS.
InterPro; IPR00550; CBS.
InterPro; IPR005170; CBC_transpt-asc.
Ffam; PP00571; CBS; 2.
Ffam; PP01595; DUP21; 1.
SMART; SM00116; CBS; 1.
Hypothetical protein; CBS domain; Repeat; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.5%; Score 33; DB 1; Length 428; 77.8%; Pred. No. 39;
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Best Local Similarity 77.8-
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92
130
128 AA;
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YA06_HUMAN
ID YA06_HUMAN
AC O60813;
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Hypothetical protein

435 AA

PRT;

STANDARD;

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30-MAY-2000 (Rel. 39, Created)

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Gaps

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MEDINE-STABLES;

MEDINE-STABLES;

MEDINE-STABLES;

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MEDINE-STABLES;

MISCHINE-STABLES;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99389880; PubMed=10460257;
Homayouni R., Rice D.S., Sheldon M., Curran T.;
"Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Identification of a mouse brain cDNA that encodes a protein related to the Alzheimer disease-associated amyloid beta protein precursor."; Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                           APPI MOUSE STANDARD; PRT; 653 AA.

003157; Q8VC38;
01-0CT-1993 (Rel. 27, Created)
11-0CT-1993 (Rel. 27, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
APLP1.
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BADLINE=93066322; PubMed=1279693;
WaSCO W. Bupp K., Magendantz M., Gusella J.F., Tanzi R.E.,
Solomon F.;
                                                                                           Match 82.5%; Score 33; DB 1; Length 500; Local Similarity 87.5%; Pred. No. 46; 7; Conservative 1; Mismatches 0; Tndele
                         500 500
500 AA; 58247 MW; 1895CDBABF14B7C3 CRC64;
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MEDLINE=96139497; PubMed=8576160;
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                                                                                                                    Query Match
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10 APP1 MOUSE

11 APP1 MOUSE

11 APP1 MOUSE

12 01-OCT-

13 AMYJOIG

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17 AMS AMS AMS

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                                                                                                                                                                                                                           OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: N. - and O-glycosylated.

MISCELLANBOUS: Binds zinc and copper in the extracellular domain.

MISCELLANBOUS: Binds zinc and copper in the extracellular domain.

MISCELLANBOUS: Binds zinc and copper in binding. No Cu(II) reducing activity with copper-binding.

SIMILARITY: Belongs to the APP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis; EndocytosIs; Cell adhesion; Coated pits; Neurone; Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
                    MEDLINE-214 (1915) PubMed-11517249; MEDLINE-214 MEDLINE-214 MEDLINE-215 PubMed-11517249; Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Haraki T., Hirai S., Ohno S., Kita Y., Kawasumi M., Kouyama K., Yamamoto T., Kyriakia J.M., Nishimoto I.; Kyriakia J.M., Nishimoto I.; C.-jun N.-terminal kinase (JNK) -interacting protein-1b/islet-brain-1 scaffolds Alzheimer's amyloid precursor protein with JNK."; (6)
                                                                                                                                                                                                                      GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBB1, AND MUTAGENESIS TYR-641.
MEDLINE=22313598; PubMed=12228233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: Proteolytically cleaved by caspases during neuronal apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMYLOID-LIKE PROTEIN 1. C30 (BY SIMILARITY).
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HSSP; P05067; IMWP.
MGD; MGI:88046; Aplpl.
InterPro; IPR008155; A4_APP.
InterPro; IPR008155; A4_extra.
Pfam; PF02177; A4_EXTRA; 1.
PROSITE; PS00030; AA_EXTRA; 1.
PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00319; A4_EXTRA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L04538; AAA37247.1; -. EMBL; BC021877; AAH21877.1; -.
[5]
INTERACTION WITH MAPKBIPL.
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN=Isolate Jari,
MEDLINE=92207142; Pubmed=1612644;
Lawlor D.A., Parham P.;
Patrancture of CD8 alpha and beta chains of the orangutan: novel
Typetterns of mRNA splicing encoding hingeless polypeptides.";
Immunogenetics 36:121-126(1922)
Immunogenetics 36:121-126(1
                                                                                                                                                                                                                                                                                                                                  CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
ENDOCYTOSIS SIGNAL.
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01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD8 alpha chain precursor (T-lymphocyte differentiation antigen T8/LEU-2).
                                                                                                                                                                                                                                                 REQUIRED FOR COPPER(II) REDUCTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craníata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
Y-9G KEDUCED BINDING OF APBB1.
P -> PP (IN REF. 2).
56516DC3EA40E480 CRC64;
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                                                                                 ZINC-BINDING (BY SIMILARITY).
HEPARIN-BINDING (BY SIMILARITY).
COLLAGEN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                           BASOLATERAL SORTING SIGNAL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 1; Length 653;
Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
  EXTRACELLULAR (POTENTIAL).
                                         CYTOPLASMIC (POTENTIAL).
COPPER-BINDING.
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                                                                                                                                                                                                                                                                       SIMILARITY)
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77. Conservative
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21 LLLPLSLLL 29
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653 AA;
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NR FIRST SESSONS CASCAGE

NR HASP, PO1732, 1CDB.

NR GO, GO.0042201; C:T-cell receptor complex; ISS.

R GO, GO.0042201; C:T-cell receptor activity ISS.

R GO, GO.0042288; F:MrC class I protein binding; ISS.

R GO, GO.000515; F:protein binding; ISS.

R GO, GO.000515; F:protein binding; ISS.

R GO, GO.000516; F:protein binding; ISS.

R GO, GO.0007169; F:T-cell activation; ISS.

R GO, GO.007169; F:T-cell activation; ISS.

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MEDLINE=86103103; PubMed=3936473;
Parres J.R., Sizer K.C., Sukhatme V.P., Hunkapiller T.;
Parres J.R., Sizer K.C., Sukhatme V.P., Hunkapiller T.;
Berricture of Leu-2/TB as deduced from the sequence of a cDNA clone.";
Behring Inst. Mitt. 77:48-55(1985);
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21-UUL-1986 (Rel. 01, Last sequence update)
21-UUL-1986 (Rel. 42, Last amortation update)
T-cell surface glycoprotein CD8 alpha chain precursor (T-lymphocyte differentiation antigen T8/Leu-2).
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T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-85099337; PubMed=3871356;
Littman D.R., Thomas Y., Maddon P.J., Chess L., Axel R.;
"The isolation and sequence of the gene encoding T8: a molecule
defining functional classes of T lymphocytes.";
Cell 40:237-246(1985).
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CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
BY SIMILARITY.
F3EC093EADB05561 CRC64;
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MEDLINE=90035142; PubMed=2509342;
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Best Local Similarity 77.8
Matches 7; Conservative
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198
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Homo sapiens (Human)
PIR; S25656; S25656.
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146
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198 AA;
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P01732;
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Mannose-binding protein A precursor (MBP-A) (Mannan-binding protein).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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MEDLINE-87222358; PubMed=3584121;
MEDLINE-87222358; PubMed=3584121;
MEDLINE-8722358; Sannoh T., Kawasaki N., Kawasaki T., Yamashina I.;
"Serum lectin with known structure activates complement through the classical pathway.";
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Drickamer K., Dordal M.S., Reynolds L.;
Mannose-binding proteins isolated from rat liver contain
carbohydrate-recognition domains linked to collagenous tails.
Complete primary structures and homology with pulmonary surfactant
                         CELL SURFACE GLYCOPROTEIN CD8 ALPHA
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                                                                     EXTRACELLULAR (POTENTIAL).
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25729 MW; FCCA29BAA73726BB CRC64;
                                                                                                                    CYTOPLASMIC (POTENTIAL). IG-LIKE V-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biol. Chem. 261:6878-6887(1986).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody.

-!- SUBDINIT: Oligomeric complex of 6 set of homotrimers.
-!- SUBCELLULAR LOCATION: THIS PROTEIN IS LOCATED INTRACELLULAR, MOST PREDOMINANTLY IN THE ROUGH ENDOPLASMIC RETICULM AND IN THE GOLGI APPARATUS, AND LITTLE OR NO MBP IS PRESENT IN PLASMA MEMBRANES AND LYSGOMES. THE MBP IS EXCLUSIVELY LOCALIZED IN THE CISTERNAL SPACE OF THE ORGANELLES, PROBABLY AS LOCOSELY BOUND MEMBRANE PROTEIN.
-!- SIMILARITY: Contains 1 collagenous domain.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Binds mannose and N-acetylglucosamine in a calcium-dependent manner. Is capable of host defense against pathogens, by activating the classical complement pathway independently of the
                                           X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 124-238.
MEDLINE=92086855; PubMed=1721241;
Weis W.I., Kahn R., Fourme R., Drickamer K., Hendrickson W.A.;
"Structure of the calcium-dependent lectin domain from a rat mannose-binding protein determined by MAD phasing.";
Science 254:1608-1615(1991).
                                                                                                                                                                                                                              X-RAY CRYSTALLCGRAPHY (1.7 ANGSTROMS) OF 124-238.
MEDLINE=93063338; PubMed=1436090;
Weis W. I., Dricksmer K., Hendrickson W.A.;
"Structure of a C-type mannose-binding protein complexed with an oligosaccharide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 90-238.
MDBLINE=99119227, Pubmed=922165,
NG K.K.-G., Park-Gryder S., Weis W.I.;
"Ca2+-dependent structural changes in C-type mannose-binding
                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 84-238.
MEDLINE=95219384; PubMed=7704532;
Weis W.I., Drickamer K.;
Wrimeric structure of a C-type mannose-binding protein.";
Structure 2:1227-1240(1994).
J. Biol. Chem. 262:7451-7454(1987),
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Biochemistry 37:17965-17976(1998)
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EMBL; M14104; AAA98781.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                        Nature 360:127-134(1992).
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31-OCT-93.
03-APR-96.
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07-FEB-95.
12-FEB-97.
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05-JUL-02.
05-JUL-02.
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LKWT;
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Gaps
                                   InterPro; IPR001860; Collagen.
InterPro; IPR001804; Lectin_C.
Pfam; PF018191; Collagen; 1.
SMART; SM00034; CLECT; 1.
PR0SITE; PS00615; C_TYPE_LECTIN_1; 1.
PR0SITE; PS00615; C_TYPE_LECTIN_2; 1.
Complement pathway; Membrane; Mannose-binding; Calcium; Repeat; Signal; Collagen; Lectin; Glycoprotein; Hydroxylation; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (Dog).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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                                                                                                                                      MANNOSE-BINDING PROTEIN A.
                                                                                                                                                         (SHORT FORM) (POTENTIAL).
                                                                                                                                                                                               HYDROXYLATION.
HYDROXYLATION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          25308 MW; 1A927482B8A8CB3D CRC64;
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01-FEB-1994 (Rel. 28, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD8 alpha chain precursor.
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                                                                                                                                               COLLAGEN-LIKE.
C-TYPE LECTIN (
HYDROXYLATION (
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STRAIN=Beagle; TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 77.8
Matches 7, Conservative
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PDB; 1KMY; 05-UUL-02.
PDB; 1KMZ; 05-UUL-02.
PDB; 1KXO; 05-UUL-02.
PDB; 1KXI; 05-UUL-02.
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238 AA;
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CD8A_CANFA
ID CD8A_CANFA
AC P33706;
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DOMAIN
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MEDLINE=91302311; PubMed=2071582;
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation. the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                               GO, GO:004211, CT-cell receptor complex; ISS.
GO; GO:0015026; F:coreceptor activity; ISS.
GO; GO:0015026; F:coreceptor activity; ISS.
GO; GO:0042515; F:protein binding; ISS.
GO; GO:0006955; F:immune response; ISS.
GO; GO:00042110; P:T-cell activation; ISS.
GO; GO:000710; P:T-cell activation; ISS.
InterPro; IPR00310; Ig-like.
     ##DULINESTRING TO CONTROL S.P., Waldmann H.;
GORMAN S.D., Frewin M.R., Cobbold S.P., Waldmann H.;
"Isolation and expression of cDNA encoding the canine CD4 and CD8
alpha antigens.";
Tissue Antigens 4.;
FUNCTION: Identifies cytotoxic/suppressor T-cells that interact
with MHC class I bearing targets. CD8 is thought to play a role in
the process of T-cell mediated killing. CD8 alpha chains binds to
class I MHC molecules alpha-3 domains.
Inthed by two disulfide bonds. Can albo form homodimers.
SUBCELLULAR LOCATION: Type I membrane protein.
SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-CELL SURFACE GLYCOPROTEIN CD8 ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL).
1018579779A5CB7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSS0835; IG LIKE; 1.
Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.0%; Score 32; DB 1; Length 239; 77.8%; Pred. No. 36; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCT1 HUMAN STANDARD; PRT; 247 AA.
P2396; Q16018;
01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
CMMAI OR CYM OR CYH.
HOMO Sapiens (Human).
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BY SIMILARITY
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MEDLINE=94378217; PubMed=8091416;
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156 156 N
239 AA; 26036 MW;
                                                                                                                                                                                                                                                      EMBL; L14287; AAB02294.1; -. HSSP; P01732; 1CD8.
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SMART; SM00406; IGv;
PROSITE; PS50835; IG
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Local 7; Conserv?
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Schechter N.M., Strobl S.,
Schechter N.M., Strobl S.,
J. Mol. Biol. 286:817-817(1999).

-!- FUNCTION: Major secreted protease of mast cells with suspected
roles in vasoactive peptide generation, extracellular matrix
degradation, and regulation of gland secretion.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Phe-|-Xaa > Tyr-|-Xaa > Leu-|-Xaa |
-!- STBCELDULAR LOCATION: Mast cells in lung, heart, skin and placenta.
-!- SIMILARITY: Belongs to peptidase family Sl. Granzyme subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE-93265916; PubMed-8495723; Sukenaga Y., Kido H., Neki A., Enomoto M., Ishida K., Takagi K., Katunuma N.; "Purification and molecular cloning of chymase from human tonsils."; PERS Lett. 323:119-122(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=99134936; Pubmed=9931257;
Pereira P.J.P., Wang Z.-M., Rubin H., Huber R., Bode W.,
Schechter N.M., Strobl S.;
Schechter N.M., Strobl S.;
The 2.2-A crystal structure of human chymase in complex with
succinyl-Ala-Ala-Pro-Phe-chloromethylketone: structural explanation
for its dipeptidyl carboxypeptidase specificity.";
J. Mol. Biol. 286:163-173(1999).
Caughey G.H., Zerweck E.H., Vanderslice P.;
"Structure, chromosomal assignment, and deduced amino acid sequence of a human gene for maet cell chymase.";
J. Bioll. Chem. 266:12956-12963 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
WEDLINES-29062883, Pubmed-2400368;
MCGrath M.E., Mirzadegan T., Schmidt B.F.;
"Crystal structure of phenylmethanesulfonyl fluoride-treated human
                                                                                                                                                                                                                                                                                                           Urata H., Kinoshita A., Perez D.M., Misono K.S., Bumpus F.M., Graham R.M., Husain A.; "Cloning of the gene and CDNA for human heart chymase."; J. Biol. Chem. 266:17173-17179(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jenne D.B., Tschopp J.;
"Angiotensin II-forming heart chymase is a mast-cell-specific
                                                                                                                                                                                                                                                                         MEDLINE=91373329; PubMed=1894611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91264818; PubMed=2049082;
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EMBL; M64263, AAA52020.1; --
EMBL; M69136; AAA52019.1; --
EMBL; X59072; CAA41796.1; --
EMBL; S6134; AAB26628.1; --
PIR; A40967; KXHUCM.
PDB; 1KLT; 13-JAN-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enzyme.";
Biochem. J. 276:567-568(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 26-60 FROM N.A.
                                                                                                                                                                                                SEQUENCE FROM N.A.
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FT STRAND 228 233 236
FT HELIX 233 236
ST HELIX 237 247
SQ SEQUENCE 247 AA; 27325 WW; DC1464A049ED6B00 CRC64;

Query Match
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps
Qy 1 LLLPLQILL 9
Db 2 LLLPLDLLL 10
Search completed: March 1, 2004, 17:29:56
Job time: 7 secs
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Query Match
100.0%; Score 40; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 9; Conservative 0; Mismatches 0; Indels
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Q8vca9 mus musculu
Q8r5d5 mus musculu
Q8r2d5 pyrococcus
Q9v2d5 pyrococcus
Q9v2d5 pyrococcus
Q9ln2d lumpy skin
Q9ln2d lumpy skin
Q9ln2d lumpy skin
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Q8xq03 salmonalla
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                                                               March 1, 2004, 17:20:41 ; Search time 30.3333 Seconds (without alignments) 93.615 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Q97H76
Q8BJK7
Q9X620
Q9D226
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2: sp-bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
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Maximum DB seq length: 200000000
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mycobacte brucella brucella	O93808 shigella il Q8xfy3 salmonella Q9hw63 pseudomonas Q8x9c3 escherichia Q9sea5 guillardia Q9x9c3 enerhanchach	Q82h48 streptomyce Q8eiy2 shewanella Q8u289 pyrococcus	Q8VD59 white spot Q8vD59 white spot Q8brv0 mus musculu	Volby, leptospila Ogckez pasteurella Ogmzyć namestra br	Q8mzx/ product ince Q8mzv6 spodoptera Q8mzz6 cydia pomon	Q13970 Mono sapien Q8taw8 homo sapien Q96qr6 homo sapien	Q9xsm6 saimiri sci Q7vht6 helicobacte Q8x6d3 escherichia	0922g5 mus musculu 08uie2 agrobacteri				date) undate)		rtebrata; Buteleostomi; Hominidae; Homo.			databases.			; IEA.						8 CRC64;
053979 QBYHY9 QBFZX1	Q83K08 Q9HW63 Q9KX3 Q9SEA5	Q82H48 Q8EIY2 Q8U289	Q8VB6 Q8VB59 Q8BRV0	Q9CKE2 Q9CKE2 Q8MZY6	QBMZV6 QBMZZ6 CBMZZ6	Q13970 Q8TAW8 Q96QR6	Q9XSM6 Q7VHT6 Q8X6D3	Q922G5 Q8UIE2	ALIGNMENTS		PRT; 253 AA.	Created) Last sequence update) Last annotation updat	cum corneum)	a; Craniata; Vertebrata s; Catarrhini; Hominida				TO PEPTIDASE FAMILY SI	sin activity, IEA. activity, IEA.	stivity, IEA. is and peptidolysis	r_trypsin. ase_S1	DR InterPro; IPR001314; Peptidase_S1A. DR Pfam; Pr00089; trypsin; 1.		OM; 1. IS; 1.	protease.	W; 2D68B6A41B22A66
2.5 294 16 2.5 370 16 2.5 370 16	82.5 399 16 82.5 413 16 82.5 426 16 82.5 428 16 82.5 470 8	22.5 516 16 22.5 547 16 20.0 58 17	0.0 72 12 0.0 79 12 0.0 102 11	0.0 150 16	0.00 182 5	0.0 235 4 0.0 235 4	0.0 235 6 0.0 242 16 0.0 249 16	0.0 256 11 0.0 264 16			PRELIMINARY;	(TremBirel, 22, TremBirel, 22, TremBirel, 25,	(chymot (Human)	tazoa; Chordat heria; Primate	606,	1 N.A.	., JN-2002) to the	TY: BELONGS TO F	33; F:chymotrype 33; F:peptidase	95; Fitrypsin ac 08; Piproteolysi	1009003; Cys Ser 1001254; Peptida	1001314; Peptide 17, trypsin; 1.	722; CHIMOIRIES	0240; TRYPSIN DO	1135; TRYPSIN SE Totease; Serine	53 A.A.; 27608 MV
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Similar to RIKEN cDNA 1110002023 gene.
Buks musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
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Mammalia, Sutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%; Score 38; DB 11; Length 73; 88.9%; Pred. No. 4.2; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Salivary gland;
Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021345; AAH21345.1; -.
SEQUENCE 73 AA; 7819 MW; 93E8F53399BF3C11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022900; AAH22900.1;
GO; GO:0006457; P.;
GO; GO:0006457; P.;
FXRP PPIASE.

Ffam; PF02254; FKBP; I.
PROSITE; PS00453; FKBP PPIASE 1; 1.
PROSITE; PS00453; FKBP PPIASE 1; 1.
PROSITE; PS00453; FKBP PPIASE 3; 1.
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to RIKBN cDNA 1110002023 gene.
FYERPI OR 1110002023RIK.
Mus musculus (Mouse)
                                                                                                                                      73 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 104 AA.
                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                      PRELIMINARY;
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s illitioliti 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                             QBVCA9;
                                                                                                                                   QBVCA9
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021527
ID 02152
AC 02152
                                                                                  ESULT 2
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RT algonodontine rodents.";

Mol. Biol. Evol. 15:35-49(1998).

RC -1-CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

C -1-CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

C -1-CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

C -1-CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

C -1-CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

C -1-CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

C -1-CATALYTIC ACTIVITY: NADH + UBIQUINONE = NADH + UBIQUINOL.

C -1-CATALYTIC ACTIVITY: NADH - UBIQUINONE = NAD(+) + UBIQUINOL.

C -1-CATALYTIC ACTIVITY: NADH - UBIQUINONE = NAD(+) + UBIQUINOL.

C -1-CATALYTIC ACTIVITY: NADH - UBIQUINONE = NAD(+) + UBIQUINONE, Nitochondrion.

C -1-CATALYTIC ACTIVITY: NADH - UBIQUINONE, NITOCHONDRIONE, NADI, OXIGONEQUICASE, UBIQUINONE, NITOCHONDRIONE, NITOCHONDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=98152303; PubMed=9491603;
Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;
"Molecular systematics and paleobiogeography of the South American
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Arvicolinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 92.5%; Score 37; DB 8; Length 208; Best Local Similarity 88.9%; Pred. No. 17; Matches 8; Conservative 1; Mismatches 0; Indels
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NADE dehydrogenase subunit 4 (EC 1.6.5.3) (NADH-ubiquinone oxidoreductase chain 4) (Fragment).
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Submitted (UUL.1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ2494283: CAB49063.1;
PIR, H75201; H75201.
InterPro; IPR008537; DUF819.
Pfam; PF05684; DUF819.
Hypothetical protein; Complete proteome.
SEQUENCE 146 AA; 16092 MW; 7182941371258C1F CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein PYRAB01390.
PYRAB01390 OR PAB0088.
Pyrococcus abyssi.
                                                                                                                                                                                               Clethrionomys gapperi (Southern red-backed vole).
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 146 AA.
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                                                                                                                                                                                                                                                                                                                                             Clethrionomys.
NCBI_TaxID=56223;
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[2]
SEQUENCE FROM N.A.
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           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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MEDLINE=21329495; PubMed=11435593;
Tulman E.R., Afonso C.L., Lu Z., Zeak L., Kutish G.F., Rock D.L.;
"Genome of lumpy skin disease virus.";
J. Virol. 75:7122-7130(2001).
     o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Neethling;
Stipinovich C., Vreede F.T., Kara P.D., Wallace D.B., Nel L.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34, DB 12; Length 162;
Pred. No. 55;
0; Mismatches 1; Indels
     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease virus genome.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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EMBL, AF40018; AMN02734.1; --
InterPro, IPR00181, Znf_ring.
Pfam, PF000097, Zf_C3HC4/1.

RYPOCherical protein, Metal-binding; Zinc; Zinc-finger.

SEQUENCE 162 AA; 18782 MW; SF914A4080F729EE CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DMC-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (LAP/PHD-finger protein).
LW010.
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     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lumpy skin disease virus (LSDV).
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LSDV010 OR LD010.
Lumpy skin disease virus (LSDV)
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Best Local Similarity 88.9%;
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7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                            |||||||::
67 LLLPLQIII 75
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                                                                                                  1 LILPROILE 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=59509;
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WEDLINE=20504483; PubMed=11016950;
WA WI, Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
WA WI, Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
WA Shukla H.D., Lasky S.P., Baliga N.S., Thorsson V., Sbrogna J.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
A Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
A leithauser B., Kreller K., Cruz R., Danson M.J., Hough D.W.,
A maddocks D.G., Jablonski P.E., Krebs M.P., Spudich J.L., Jung K.-H.,
I senbarger T.A., Peck R.P., Pohlschroder M., Spudich J.L., Jung K.-H.,
Adam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Adam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Adam M. Andl. Acad. Sci. Us. A. 97:12176-12181(2000).

EMBL, AEGOSO72; AAG19641.; -.
DR C. G.: Greenbrane, IEA.
DR G. G.: Greenbrane, IEA.
DR G.: Greenbrane, IEA.
DR G.: Greenbrane, IEA.
DR G.: Greenbrane, IEA.
DR Ffm., PFO2628; COXIS_CraA.; 1.
Complete proteome.
SQUENCE 277 AA; 29053 MW; B053123766E274B1 CRC64;
                                                                                                                                      0; Gaps
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STRAIN-Meethling 2490;
Tulman B.R., Affonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
Submitted (AUG-2001) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

85.0%; Score 34; DB 12; Length 162;
Best Local Similarity 88.9%; Pred. No. 55;

Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match
Local Similarity 66.7%; Pred. No. 90;
Local Similarity 66.7%; Pred. No. 90;
Local Scholarity 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 277 A.A.
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97 VLLPLOVIL 105
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Query Match
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Q8Z802;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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"Bovine surfactant protein D: Genomic characterization, chromosomal rocalization and tissue distribution.";

"Bovine surfactant protein D: Genomic characterization, chromosomal rocalization and tissue distribution.";

"Bowline MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL: AJ548848; CAD69922.1;

EMBL: AJ548849; CAD69922.1;

EMBL: AJ548850; CAD69922.1;

EMBL: AJ548850; CAD69922.1;

Interpro; IPR001304; Calagen.

R Interpro; IPR001304; Cetin.C;

Pfam: PF001391; Collagen;

R Pfam: PF00159; Lectin.C;

R Pfam: PF00159; CayPE_LECTIN 1;

R PROSITE; PS00613; CTYPE_LECTIN 2;

R PROSITE; PS00613; CTYPE_LECTIN_2;

R PROSITE; PS00613; CTYPE_LECTIN_2;
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STRAIBLIZ / ASC2 700720;
STRAIBLIZ / GSSC112 / ATCC 700720;
MCDLINE-21534948; PubMed=11677609;
MCCLelland M., Sanderson K.E., Spieth J., Cliffton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Soctt K., Holmes A., Grewal N., Milvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.0%; Score 34; DB 6; Length 369; 77.8%; Pred. No. 1.2e+02; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        surfactant protein D.
surfactant protein D.
; 4A74B7593508AESD CRC64;
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01-JUN-2003 (TrEMBirel. 24, Last sequence update)
01-0CT-2003 (TrEMBirel. 25, Last annotation update)
Surfactant protein D precursor:
                                                                                           369 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 20 PG
21 67 B1
245 369 B1
369 AA; 37405 MW;
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EMBL; AE008742; AAL19917.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 77.8 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae, Bovinae, Bos.
NCBI_TaxID=9913;
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                                                                                                                       Q863A1;
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                        38ULT 9
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G. Sebaihia M., Backser S., Basham D., Brocks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davise R.M., Dowd L., White N., Fazrar J., Riogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Mhitehead S., Barrell B.G.; Simmonds M., Skelton J., Stevens K., Mhitehead S., Barrell B.G.; auultiple drug resistant salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAINS-Z2531367, ATCC 700931; BMEDLINE-Z2531367, PubMed=15644504; Deng W., Liou S.-R., Plunkett G. III, Maynew G.F., Rose D.J., Burland V., Kodoylanni V., Schwartz D.C., Blattner F.R.; and Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last annotation update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
STY0984 OR YOAL OR T1951.
STY0984 OR YOAL OR T1951.
STRONGHIA: Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 85.0%; Score 34; DB 16; Length 754; Local Similarity 77.8%; Pred. No. 2.3e+02; Pred. No. 2.2e+02; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 754;
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TIGRRAMS; TIGR00360; ComEC N·term; 1.
TIGRPAMS; TIGR00361; ComEC Nec2; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 754 AA; 84954 NW; 711A95D282271358 CRC64;
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EMBL, AE016840; AA069565.1; --
GO; GO:0016621; C:integral to membrane; IEA.
GO; GO:030420; P:establishment of competence
InterPro; IPR004279; Blactmase-like.
InterPro; IPR004477; ComEC_N-term.
InterPro; IPR004977; ComEC_N-term.
GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0039420; Prestablishment of competence InterPro; IPR001279; Blactmase-like.
InterPro; IPR004477; COMEC_N-term.
InterPro; IPR004477; COMEC_Necz.
InterPro; IPR004797; COMEC_Necz.
Plam; PR03772; COMPCELONC; I.
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO SEA / DSW 792 / VKM B-1787;

MADDINE=21359325; PubMed=11466286;

MADDINE=21359326; PubMed=11466286;

MADDINE=21359326; PubMed=11466286;

MADDINE=21359326; PubMed=11466286;

MADDINE=21359326;

MADDINE=21359326;

MADDINE=21359326;

MADDINE=213593366;

MADDINESPERSE=11676669;

MADDINESPERSE=11676669;

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MADDINESPERSE=1167669;

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MADDINESPERSE=1167699;

MADDINE
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                                                                                                                                                                                                                                                                                                                              Clostridium acetobutylicum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 85.0%; Score 34; DB 16; Length 845; Best Local Similarity 97.5%; Pred. No. 2.5e+02; Matches 7; Conservative 1; Mismatches 0; Indels
Best Local Similarity 77.8%; Fred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
SEQUENCE 845 AA; 93779 MW; 401293AA1FF9D757 CRC64;
                                                                                                                                                                                                                                 01-0CT-2001 (TrEMBLrel 18, Created)
01-0CT-2001 (TrEMBLrel 18, Last sequence update)
01-0CT-2003 (TrEMBLrel 25, Last annotation update)
Cation transport P-type ATPase.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
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                                                                                              371 LLLPLOVAL 379
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Q8BJK7
ID Q8BJK
AC Q8BJK
DT 01-MAI
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SEQUENCE FROM N.A.
STRAM=CSPRIAL(64); TLSUB=Body;
STRAM=CSPRIAL(65); PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team,
the RIKEN Genome Exploration Research Group Phase I & II Team,
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-langth cDNAs.";
Nature 420:583-573(2002).
BARL, AK083529; BAC38942.1; -
SEQUENCE 109 AA; 12276 MW; B52E75D4571F8DC6 CRC64;
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01-070-2001 (TrEMBLrel. 17, Last sequence update)
01-071-2003 (TrEMBLrel. 25, Last annotation update)
4030007E1981K, Protein.
4030007E1981K, Mouse).
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muribae; Musinse; Mus.
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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Enterobacteriaceae, Salmonella,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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EMBL; AF1308F7; AAD31438.1; -...
PinterPro; IPR002550, CSS.
Pfem; PP0;1595; DUE21; 1.
SEQUENCE 196 AA; 21859 MM; B06659F7E5BAAITA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nery Match 82.5%; Score 33; DB 11; Length 109; lest Local Similarity 66.7%; Pred. No. 60; Atches 6; Conservative 3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel, 12, Created)
01-NOV-1999 (TrEMBLrel, 12, Last sequence update)
01-JUN-2003 (TrEMBLrel, 24, Last annotation update)
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Query Match 82.5%; Score 33; DB 11; Length 196; Best Local Similarity 77.8%; Pred. No. 1e+02; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                Chaperone; Repeat.
SEQUENCE 196 AA; 17777 MW; 2136738FD496D815 CRC64;
NCBI_TaxID=10090;
                                                                                                                   SEQUENCE
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Search completed: March 1, 2004, 17:34:44 Job time: 32.3333 secs

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0; Gaps

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March 1, 2004, 17:21:46; Search time 11.8889 Seconds (without alignments) 39.081 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                           otal number of hits satisfying chosen parameters:
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                                                                               4 protein - protein search, using sw model
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries finimum DB seq length: 0

Issued\_Patents\_AA:\*
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2: /cgn2 6/pcdata/2/iaa/5A\_COMB.pep:\*
3: /cgn2 6/pcdata/2/iaa/6A\_COMB.pep:\*
4: /cgn2 6/pcdata/2/iaa/6B\_COMB.pep:\*
5: /cgn2 6/pcdata/2/iaa/PcTUS\_COMB.pep:\*
6: /cgn2 6/pcdata/2/iaa/PcTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		App1	Appl	Appli	Appl	Appl	Appli	Appl	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appli	Appl:	Appl	Appl	App1	Appl	Appl	23425	Appl	Appl	Appl	Appl	Appl
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		02-6	18-2		1	57-1	27-3	54-3	44-6	4-	1	24-	54-3	30-1	10-	64-	9	4	502-6	å	8	4	80	85-4	œ	84-	0	9-90
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	QI	US-0	us-0	us-o	us-o	US-0	US-0	us-o	0-SD	us-o	US-0	08-0	US-0	ns-o	us-0	0s-0		us-o	US-0	us-o	<b>US-0</b>	US-0	5223	0.80	US-0	US-0	US-0	us-o
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Appl	Appl	Appl	Appl	Appl	Appl	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl
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Segnence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Seguence
US-08-817-795-75		-08-639	US-09-012-431-75	US-09-012-692-75	US-08-906-613-75	PCT-US95-14442A-75	US-08-485-455D-17	US-08-482-130C-17	US-08-484-211C-17	US-08-817-795-17	US-08-485-443B-17	PCT-US95-14442A-17	•	US-08-906-616-17	US-08-639-075A-17	US-09-012-431-17	US-09-012-692-17
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28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

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RESULT 1
US-005-602-600-34
US-005-602-600-34
Sequence 34, Application US/09502600A
Patent No. 6294344
| GENERAL INFORMATION:
APPLICANT: 0'Brien, Timothy J.
ITILE OF INVENTION: Compositions and Methods for the Early Diagnosis of TILLE OF INVENTION: O'Arrian Cancer
| TILLE OF INVENTION: Compositions and Methods for the Early Diagnosis of FILE REFERENCE: D6223CIP-C
| CURRENT PILING DATE: 2000-02-11
| CURRENT APPLICATION NUMBER: 09/039,211
| PRIOR PILING DATE: 03-14-1998
| NUMBER OF SEQ ID NOS: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Residues 58-66 of the SCCE protein US-09-502-600-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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0; Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels

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1 VLVNERWVL 9 

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APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
TITLE ON: INVENTION: Methods for the early diagnosis of ovarian cancer FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 34 Sequence 34, Application US/09918243 Patent No. 6627403 GENERAL INFORMATION: US-09-918-243-34 LENGTH: RESULT 2

TYPE: PRT ORGANISM: Homo sapiens

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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-944-483-33
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US-08-557-146-12
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APPLICANT COHEN, MAURICE
APPLICANT COLEN, TRACEY L.
APPLICANT FRIEDMAN, PAULA N.
APPLICANT FRIEDMAN, PAULA N.
APPLICANT FRIEDMAN, PAULA N.
APPLICANT FRIEDMAN, PAULA N.
APPLICANT FRIEDMAN, STEWARD N.
APPLICANT STEWER, STEVEN D.
APPLICANT STEWER, OF THE PROSTATE
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS: 76
CORRESPONDENCE ADDRESS: 76
CORRESPONDENCE ABOORT LABORATORIES
STREET: 100 Abboct Laboratories
STREET: Abbott Park Road
                                                                                                                                                                                                                                                                                                                                             ESULT 3
19-00-261-416-7
19-00-261-416-7
Sequence 7, Application US/09261416A
Sequence 7, Application US/09261416A
Sequence 7, Application US/09261416A
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: TAGG-12: A No. 6291663el Transmembrane Serine Protease
FILE REFERENCE: D6192
FURRENT APPLICATION UNMBER: US/09/261,416A
CURRENT APPLICATION UNMBER: US/09/261,416A
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Serine proteage catalytic domain of stratum corneum OTHER INFORMATION: chymotryptic enzyme (Scce) homologous to similar OTHER INFORMATION: domain in TADG-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                  Query Match 100.0%; Score 47; DB 4; Length 9; Best Local Similarity 100.0%; Pred. No. 38+05; Matches 9; Conservative 0; Mismatches 0; Indels
                      NAME/KEY: CHAIN
CTHERNATION: Residues 58-66 of the SCCE protein
3-09-918-243-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 33, Application US/08944483; Patent No. 6232456
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Best Local Similarity 100.0
Matches 9; Conservative
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ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VLVNERWYL 12
                                                                                                                                                                                                                                                         1 VLVNERWYL 9
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US-08-944-483-33
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FEATURE:
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0; Gaps
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Fatent No. 5834290
GENERAL INFORMATION:
APPLICANT: Egelson, Lenart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 47; DB 3; Length 224; Best Local Similarity 100.0%; Pred. No. 0.43; Matches 9; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIPICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: White & Case, Patent Department STRET: 1155 Avenue of the Americas STRET: New York STATE: New York
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
                                                                                                                                                                                 FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: BECKET, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECHONICATION INFORMATION:
TELEPHAN: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1103326-181
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Sterier, Stichard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 110
TELECOMUNICATION INFORMATION:
TELECPHONE: (212) 819-883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                               INPORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTERISTICS: LENGTH: 224 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
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TYPE: amino acids
STRANDEDNESS: single
                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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: U.S.A.
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CLASSIFICATION:
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US-09-654-600A-4
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Patent No. 597266
GENERAL INCORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: FALCOSIN:
TITLE OF INVENTION: Pacast and Ovarian Carcinomas
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
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OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to
OTHER INFORMATION: similar domain in TADG-15
                                                                                                                                                   0; Gaps
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APPLICANT: Bgelrud, Torbjorn
APPLICANT: Hansenon, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Bnzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                Query Match 100.0%; Score 47; DB 2; Length 225; Best Local Similarity 100.0%; Pred. No. 0.43; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 47; DB 2; Length 225; Best Local Similarity 100.0%; Pred. No. 0.43; Matches 9; Conservative 0; Mismatches 0; Indels
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STRET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
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APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
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; Patent No. 5981256
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                            30 VLVNERWYL 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Unknown
                                                      -08-557-146-12
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APPLICANT: Tanimoto, Hirotoshi
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TAGGILS: An Extracellular Serine Protease
TITLE OF INVENTION: O'VERAPAESSEG in Carcinomas
TITLE REPERRENCE: D6064CIP/D
CURRENT PAPLICATION NUMBER: U5/9/644,600
CURRENT FILING DATE: 1999-10-20
PRIOR PILING DATE: 1999-10-20
PRIOR PILING DATE: 1998-10-20
INMBER OF SEQ ID NOS: 98
SEQ ID NO 4
IENGTH: 225
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Jeguence 4, Application US/09654600A

Jeguence 4, Application US/09654600A

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Tanimoto, Hirotoshi

TITLE OF INVENTION: Tange-1s.

FILE REFERENCE: D6064CIP/D

CURRENT APPLICATION NUMBER: US/09/654,600A

FURNERY PILING DATE: 2000-09-01

FRIOR APPLICATION NUMBER: 09/421,213
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100.0%; Score 47; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 47; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels
ATTORNEY/AGENT INFORMATION:
NAME: Stefrer, Richard J.
REGISTRATION NUMBER: 35-372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMOTIOTATION INFORMATION:
TELEPRENCE (212) 819-8783
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acids
STRANDEDNESS: single
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; Patent No. 6451500
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear ; MOLECULE TYPE: polypeptide US-09-154-344-12
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US-09-644-600-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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RESULT 12
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Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Bellud. Torbjorn
APPLICANT: Hansson, lennart
ITILE OF INVENTION:
Recombinant Stratum Corneum Chymotryptic
ITILE OF INVENTION:
CORRESPONDENCE: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1158 Avenue of the Americas
CITY: New York
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
GOMPUTER: TBM PC Compatible
COMPUTER: BADABLE FORM:
MEDIUM TYPE: TORPY disk
COMPUTER: Dai-control Department
COMPUTER: Dai-control 
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100.0%; Score 47; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels
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APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
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REGISTRATION NUMBER: 35,372
REPERSNCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 354-813
INPORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 253 amino acids TYPE: amino acid TOPDE: Amino TOPDE: Amino acid TOPDE: Amino Amino TOPDE: Amino Amino TOPDE: Ami
09/027,337
PRIOR FILING DATE: 1999-10-20
1998-02-20
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 4
LENGTH: 225
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US-08-824-874-3
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IS-08-557-146-2
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Patent No. 5991256

GENERAL INPORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Earyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Match 100.0%; Score 47; DB 2; Length 253; Local Similarity 100.0%; Pred. No. 0.49; es 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FasteRO for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
FILING DATE: Filed Herewith
APPLICATION NUMBER: 51,749
FILING DATE: APPLICATION NUMBER: BILLINGS, LUCY J.
RAPLICATION NUMBER: 36,749
RESERANCE/DOCKET NUMBER: PF-0252 US
TELEPRHONE: 415-85-055
INFORMATION: FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amito acids
TTPE: amino acid
STRANDENNESS: anigle
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Sequence 3, Application US/08824874
Patent No. 5962300
GENERAL INNOVAMION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL KALLIKREIN
INVERS OF SEQUENCES:
CORRESPONDENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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CLONE: 532504
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                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                         COUNTRY:
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100.0%; Score 47; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09210084
; Sequence 3, Application US/09210084
; Patent No. 6195511
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L. APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
ADDRESSES: Incyce Pharmaceuticals, Inc. STREET: 3174 Porter Drive
CITY: Palo Alto
CITY: Palo Alto
COMPUTER: CA
ZIP: 94304
ZIP: 94304
                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. (
Matches 9; Conservative 0; Mismatch
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-05
TELECOMMUTICATION INFORMATION:
TELEPHONE: 415-85-055
TELEPHONE: 415-845-416
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
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TYPE: amino acid
STRANDEDNESS: single
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-188-2
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; CLONE: 532504
US-09-210-084-3
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US-09-764-762-3
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Patent No. 6093397
GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Dixtle, Sheila P.
TITLE OF INVENTION:
RELATED NUCLEIC ACIDS
TOWNERS PROMENCES:
ADDRESSEE: Eli Lilly and Company
STRET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTY: United States of America
STATE: Indiana
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EM PC Compatible
COMPUTER: IM PC Compatible
COMPUTER: IM PC Compatible
COMPUTER: IM PC Compatible
COMPUTER: IM PC Compatible
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                        CURRENT APPLICATION DATA: PC-LOSyMS-LOS
SOFTWARE: PETENTIN RELEASE #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: VS/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRICE APPLICATION:
PRICE APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION NUMBER: 35,372
REGISTRATION NUMBER: 35,372
REPERPENDE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.49;
Lag 0; Indels
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Best Local Similarity 100.0%; Pred. No. 4
Matches 9; Conservative 0; Mismatche
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
          PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION TELEPHONE: 317-277-1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 354 8113
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-09-154-344-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VLVNERWVL 9
          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Sequence 3, Application US/09764762

Parent W. 6472150.

GENERAL INPORMATION:

GENERAL INPORMATION:

AITUE OF INVENTION:

CORRESPONDER ADDRESS:

CORRESPONDER ADDRESS:

CONTRY: USA ALC

CITY: PALO ALC

CITY: PALO ALC

CITY: PALO ALC

CONTRY: USA COMPACINE PORM:

MEDIUM TYPE: Disket be windows Version 2.0

PRIOR DATE: 10-200.

PRIOR DATE: 10-200.

PRIOR DATE: 10-200.

PRIOR PALICATION NUMBER: 05/49

RECHERAL ON THE NUMBER: 05/49

RECHERAL ON THE NUMBER: 05/49

RECHERAL SILINGS. LULY J.

RECHERAL SILINGS. SILIGE

INMEDIUM SILINGS. SILIGE

INMEDIUM SILINGS. SECUENTIAL SILINGS.

JOHN TOPOLOGICAL HINDAR SILINGS.

JOHN TOPOLOGICAL SILINGS.

JOHN TOPOL
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Search completed: March 1, 2004, 17:38:24 Job time: 12.8889 secs

1 VLVNERWYL 9 ||||||||| 58 VLVNERWYL 66

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(without alignments) 55.820 Million cell updates/sec
                                                                                                                                                              March 1, 2004, 17:16:55 ; Search time 45.5556 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                         protein - protein search, using sw model
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US-09-905-083-34 .tle: irfect score:

Gapop 10.0 , Gapext 0.5 1 VLVNERWYL 9 **BLOSUM62** coring table: squence:

1586107 segs, 282547505 residues earched:

otal number of hits satisfying chosen parameters:

inimum DB seq length: 0 laximum DB seq length: 2000000000

Listing first 45 summaries ost-processing: Minimum Match 0%

geneseqp2000s:\* geneseqp2001s:\* geneseqp2003s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2003bs:\* A Geneseq 29Jan04:\* 1: geneseqp1980s:\* 2: geneseqp1990s:\* Jatabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	O.	374	Abg23378 Novel hum	Ada05738 Human NOV	Ada05736 Human NOV	44	Aab98502 Human Str	Ada05742 Human NOV	Ada05732 Human NOV	Ada05734 Human NOV	Aar67888 Human str	3 Human	Abb84421 Human SCC	6 Human	O Amino ac	0 Protein	Abu07471 Protein d	Abr58471 Human str	Adb80484 Ovarian c	Aab21326 Human HSC	Aae08245 Human str	Aae08255 Human str	Abb84419 Bovine SC	4420 Porcine	Aay28590 Human Fac	
ΙD	AE082	ADA05740	ABG23378	ADA05738	ADA05736	ADA05744	AAB98502	ADA05742	ADA05732	ADA05734	AAR67888	AAW05383	ABB84421	ABB84406	AAU82740	ABU07440	ABU07471	ABR58471	ADB80484	AAB21326	AAE08245	AAE08255	ABB84419	ABB84420	AAY28590	
DB	4	9	4	9	9	φ	4	ø	φ	v	~	(7	Ŋ	'n	'n	9	9	v	7	m	4	4	Ŋ	'n	7	
Length	6	97	136	181	198	224	225	247	250	252	253	253	253	253	253	253	253	253	253	257	σ	σ	243	249	212	
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Score	47	47	47	47	47	47	47	47	47	47	47	47	47	747	47	47	47	47	47	47	43	43	40	40	39	
Result No.		7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18		20				24	25	

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AAE39994	AAR05421	AAE39992	AAW01196	AAB50593	ABG75788	AAW01165	AAB50561	AAW64261	AAW10694	AAW12393	ABBS7219	AAW46773	AAG79000	AAW41955	ABB60343	ADA50480	AAW41954	AAW41953	ADB97555
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228	250	253	64	64	81	223	224	232	260	260	260	233	233	237	243	247	258	258	271
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6 8	39	о М	38	38	38	38	38	38	38	38	38	37	37	37	37	37	37	37	37
26	27	28	Ω σ	30	31	32	33	34	35	36	37	38	6 6	40	41	42	43	4	4.5

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The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCB). Proteases are considered to be an integral part of tumour growth and metastisis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
                                                                                                                                                      Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.
                                                                                                                             Human stratum corneum chymotrypsin enzyme peptide #3 (residues 58-66).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing cancer comprises detecting stratum corneum chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; Page 103; 127pp; English.
                              AAE08239 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                              07-FEB-2001; 2001WO-US003977.
                                                                                                                                                                                                                                                                                                                                                              11-FEB-2000; 2000US-00502600.
                                                                                                01-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             (UYAR-) UNIV ARKANSAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-514676/56.
                                                                                                                                                                                                                                                              WO200159158-A1.
                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                               16-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                              O'brien IJ;
                                                                 AAE08239;
RESULT 1
                   AAE08239
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Sequence 9 AA;

Query Match

100.0%; Score 47; DB 4; Length 9;

ô Dipippo VA; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Eliearman K, Malyankar UM; Obt T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton D; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Elsen AJ, Gangolli EA, Rieger DK, Spaderna SK; immunomodulator; cytostatic; notropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obseity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia. Gaps ò human; NOVX; antidiabetic; anorectic; antibacterial; vírucide; 0; Indels Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 9; Conservative 0; Mismatches 0; Human NOV18e protein SEQ ID NO:100. ADA05740 standard; protein; 97 AA. 09-OCT - 2001, 200105-0327919F.
09-OCT - 2001, 200105-0328049F.
09-OCT - 2001, 200105-0328049F.
09-OCT - 2001, 200105-0328049F.
15-OCT - 2001, 200105-0328049F.
15-OCT - 2001, 200105-0328049F.
15-OCT - 2001, 200105-0328049F.
16-OCT - 2001, 200105-0330414F.
17-OCT - 2001, 200105-0330414F.
18-OCT - 2001, 200105-0330418F.
24-OCT - 2001, 200105-034309F.
19-AFR- 2002, 200205-0373816F.
19-AFR- 2002, 200205-0373816F.
19-AFR- 2002, 200205-0373816F.
16-MAY- 2002, 200205-037381642F.
16-MAY- 2002, 200205-0381037F.
16-MAY- 2002, 200205-0381037F.
16-MAY- 2002, 200205-0381037F.
17-MAY- 2002, 200205-0381038F.
17-MAY- 2002, 200205-03813381F.
25-MAY- 2002, 200205-0381335F.
25-MAY- 2002, 200205-0381335F.
25-MAY- 2002, 200205-0381335F. 02-OCT-2002; 2002WO-US031373. 06-NOV-2003 (first entry) (CURA-) CURAGEN CORP. 1 VLVNERWVL 9 1 VLVNERWYL 9 WO2003029424-A2. Homo sapiens. ADA05740; 25740

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The present invention describes NoVX proteins, where X can be 1 to 55 (e.g. NOVY). Also described: (1) a composition comprising a polypeptide described above and a carribed; (2) a kit comprising, in one or more described above and a carribed above; (3) an isolated mucleic acid containers, the composition described above; (4) an isolated mucleic acid molecule described above; (5) a cell mount of the above polypeptide described above; (6) a cell comprising the nucleic acid molecule described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above copypeptide or nucleic acid molecule in a first mammalian subject; (9) a mample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for apthology associated with the polypeptide; (12) a method for sortening for a modulator or apthology associated with the polypeptide; (13) a method of cor identifying a pathology associated with the above polypeptide. Novy correctivity of the polypeptide described above polypeptide in a method for protective, antipacted in a method for protective, antipacted and antilipaemic activity of the polypeptide above polypeptide in a method for protective, neuroprotective, antipacting of syndrome associated with a human disease. The polypeptide or the mucleic acid molecule may be used to diagnose, treat or prevent metabolic conditions. The present expressence and various plantancement invention. The present expressence and present express
                                                                     New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                Claim 1; Page 171; 586pp; English.
WPI; 2003-381626/36.
N-PSDB; ADA05739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 97 AA;
```

100.0%; Score 47; DB 6; Length 97; 100.0%; Pred. No. 0.87; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity lov..

Best Local 9; Conservative 1 VLVNERWVL 9

ö

0; Gaps

ABG23378 standard; protein; 136 AA. 18-FEB-2002 (first entry) 39 VLVNERWYL 47 RESULT 3

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder. Novel human diagnostic protein #23369. 

Homo sapiens.

WO200175067-A2.

11-OCT-2001.

10-APR-2003

```
The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, only more and gene mapping, and in recombinant production of (II). The polynuclectides are also used in dispossites as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is oblypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging to supplement. (II) and its binding partners are useful in medical imaging involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in the protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in the cappendance other types of data and products dependent on DNA and amino acid sequences. ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGOONIO-ABGO
                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 53737; 103pp; English.
                                                                                                                                                                                                                                                                           Tang YT;
                                                          30-MAR-2001; 2001WO-US008631.
                                                                                                                    31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VLVNERWVL 9
                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73.
N-PSDB; AAS87565.
                                                                                                                                                                                                                                                                           Drmanac RT, Liu C,
                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 136 AA;
```

Ouery Match
100.0%; Score 47; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

64 VLVNERWYL 72

ADA05738 standard; protein; 181 AA. ADA05738; RESULT 4 ADAOS738
XX
XX
ADA
XX
XX
DT
DT
XX
XX
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ADA
X

Human NOV18d protein SEQ ID NO:98. 06-NOV-2003 (first entry)

immunomodulator; cytostatíc; notropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obseity; infection; cachexia; cancer; neurodegenerative disorder; Alzhaimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia. human; NOVX; antidiabetic; anorectic; antibacterial; virucide;

Homo sapiens.

24-OCT-2001, 20010S-03452895.
29-OCT-2001, 20010S-0345529F.
29-OCT-2001, 20010S-0345529F.
17-APR-2002, 20020S-0373250P.
19-APR-2002, 20020S-0373817P.
19-APR-2002, 20020S-0373817P.
19-APR-2002, 20020S-0373847P.
22-APR-2002, 20020S-0373847P.
16-MAY-2002, 20020S-0381037P.
16-MAY-2002, 20020S-0381038P.
17-MAY-2002, 20020S-0381038P.
16-MAY-2002, 20020S-0381038P.
22-MAY-2002, 20020S-038163P.
22-MAY-2002, 20020S-0381642P.
23-MAY-2002, 20020S-0381642P. 09-0CT-2001; 2001US-0328029F. 09-0CT-2001; 2001US-0328044P. 12-0CT-2001; 2001US-0328849P. 15-0CT-2001; 2001US-0328449P. 17-0CT-2001; 2001US-0329442P. 18-0CT-2001; 2001US-0330442P. 18-0CT-2001; 2001US-0330309P. 22-0CT-2001; 2001US-0341638P. 25-JUN-2002; 2002US-0391335P. 02-OCT-2002; 2002WO-US031373 (CURA-) CURAGEN CORP. 05-OCT-2001;

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36. N-PSDB; ADA05737 New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

Claim 1; Page 171; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 described above and a carrier; (2) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the mucleic acid molecule described above; (5) a vector comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the prospection of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above to lidentifying an agent that binds to the polypeptide described method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to

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the activity of the polypeptide, (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. Now, sequences have antidabetic, anotoroid; antibacterial, virucide, immunomodulator, cytostatic, nootropic, antibacterial, virucide, and antilippemic attivities, and can be used in gene therapy. The collapseptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic acid molecule may be used to diagnose, treat or prevent metabolic acid molecule may be used to diagnose, treat or prevent metabolic acid molecules such as Alzheimer's disease or Parkinson's disease, immune disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various probes, in chromosome mapping, tissue typing, preventive medicine and parmacogenomics. The present sequence represents a human NoVX from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention.
              តតកក្តុត្តស្តីក្តុស្ត្រក្តុម្ភិត្តិស្ត្
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Sequence 181 AA;

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0; Gaps
        100.0%; Score 47; DB 6; Length 181; 100.0%; Pred. No. 1.7; ative 0; Mismatches 0; Indels
1 VLVNERWVL 9
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39 VLVNERWVL 47

immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia. human; NOVX; antidiabetic; anorectic; antibacterial; virucide;

WO2003029424-A2.

ADA05736 standard; protein; 198 AA. Human NOV18c protein SEQ ID NO:96. 05-OCT-2001, 20010S-0327435P.
05-OCT-2001, 20010S-03274435P.
09-OCT-2001, 20010S-0328044P.
09-OCT-2001, 20010S-0328044P.
09-OCT-2001, 20010S-0328044P.
09-OCT-2001, 20010S-0328044P.
12-OCT-2001, 20010S-0329414P.
17-OCT-2001, 20010S-0339414P.
18-OCT-2001, 20010S-0339405P.
24-OCT-2001, 20010S-0349659P.
24-OCT-2001, 20010S-0349659P.
25-OCT-2001, 20010S-0349659P.
01-NOV-2001, 20010S-0349559P. 02-OCT-2002; 2002WO-US031373 19-APR-2002; 2002US-0373815P 06-NOV-2003 (first entry) Homo sapiens ADA05736

ADA05736

AC ADAO

XX ADAO

XX ADAO

DT 06-N

XX Huma

XX Huma

XX Huma

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on G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; ajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Gorman L, Zerkusen BD, Anderson DW, Zhong M, Carterton E; Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; ts RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; AJ, Gangolli EA, Rieger DK, Spaderna SK;
                    16-MAY-2002, 200205-0381037P.

16-MAY-2002; 200205-0381037P.

16-MAY-2002; 200205-0381042P.

17-MAY-2002; 200205-0381642P.

28-MAY-2002; 200205-0381656P.

29-MAY-2002; 200205-038181P.

25-UJN-2002; 2002US-0391335P.

01-OCT-2002; 2002US-0391335P.
2002US-0373826P.
                                                                                            (CURA-) CURAGEN CORP.
                                                                                                                                                                WPI; 2003-381626/36.
                                                                                                                 Patturajan M,
                                                                                                                                Ji W, Miller
Shimkets RA,
                                                                                                           Smithson G,
                                                                                                                                                  Eisen AJ,
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pharmacogenomics.

N-PSDB; ADA05735.

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or

Claim 1; Page 170; 585pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit composition or more containers, the composition described above; (3) an isolated nucleic acid containers, the composition described above; (5) a notainers, the composition of the invention; (4) a vector comprising the above vector; (6) an antibody that immunospecifically comprising the above vector; (6) an antibody that immunospecifically by instance or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a delace or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic described above; (10) a method for identifying a potential therapeutic agent for compression or a disease associated with altered levels of the polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological intracactions of the polypeptide; (11) a method of creening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for medial or or preventing a pathology associated with the above polypeptide; (12) and method for medial and (14) a method for protectic, and that can be associated with the above polypeptide; (12) and antilipaemic activities, and can be used a bove polypeptide; and antilipaemic activities, and can be used a bove polypeptide in a method for protectic, and antilipaemic activities, and can be used a prevent metabolic controller and antilipaemic acidities on obesity, infections, candersay, the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, and preventive metabolic controller in a protections, cachexia, and antilipaemic present invention.

Sequence 198 AA;

Gaps . 0 100.0%; Score 47; DB 6; Length 198; 100.0%; Pred. No. 1.9; tive 0; Mismatches 0; Indels 0; Mismatches 9; Conservative Query Match Best Local Similarity Matches

ADA05744 standard; protein; 224 AA.

(first entry) 06-NOV-2003

Human NOV18g protein SEQ ID NO:104.

human, NOVX, antidiabetic; anorectic, antibacterial; virucide, immunomodulator; cytostatic; nootropic; neuroprotective, antiparkinsonian, antilipaemic, gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.

WO2003029424-A2.

02-OCT-2002; 2002WO-US031373

05-OCT-2001, 2001US-0327435P.
05-OCT-2001, 2001US-0327435P.
09-OCT-2001, 2001US-0327435P.
09-OCT-2001, 2001US-0328044P.
09-OCT-2001, 2001US-0328044P.
09-OCT-2001, 2001US-0328044P.
12-OCT-2001, 2001US-0328044P.
17-OCT-2001, 2001US-0339142P.
17-OCT-2001, 2001US-0339142P.
18-OCT-2001, 2001US-0349142P.
18-OCT-2001, 2001US-034916P.
24-OCT-2001, 2001US-034916P.
19-APR-2001, 2001US-034917P.
19-APR-2002, 2002US-0373817P.
19-APR-2002, 2002US-0373817P.
19-APR-2002, 2002US-0373817P.
16-MAY-2002, 2002US-0373817P.
16-MAY-2002, 2002US-0373817P.
16-MAY-2002, 2002US-0373816P.
17-MAY-2002, 2002US-0373817P.
16-MAY-2002, 2002US-0373816P.
17-MAY-2002, 2002US-0373816F.
17-MAY-2002, 2002US-0373816F. 

(CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterron E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CBA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI: 2003-381626/36. N-PSDB; ADA05743 New NOVX polypeptides and nucleic acids, useful for diagnosing,

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOVI). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the above vector; (6) an antibody that immunospecifically breample; (6) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for abore; (10) a method for identifying a potential therapeutic agent for above; (11) a method for activitions of the polypeptide; (12) a method for modulating or pathology associated with the polypeptide; (12) a method for modulating a pathology associated with the polypeptide; (12) and (14) a method for protectic, antibacterial, virucide, mammal; and (14) a method for producing the above polypeptide in a sequences have antidiabetic, anorectic, antibacterial, virucide, and antilipaemic activities, and can be used an appropredering a medicament for treating a spathology associated with a human disorders such as diabetes or obesity, inferiors, cancer and various or disease, immune disorders such as Alpheimer's disorders such as diabetes or obesity, inferiors, care or proventive medical and antilipaemics. The present sequence re preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or Claim 1; Page 172; 586pp; English. present invention. pharmacogenomics.

Sequence 224 AA;

ö 100.0%; Score 47; DB 6; Length 224; 100.0%; Pred. No. 2.2; tive 0; Mismatches 0; Indels 0; Gaps Ouery Match
Best Local Similarity 100.0

44 VLVNERWVL 52 1 VLVNERWVL 9 d

RESULT 7

AAB98502 standard; protein; 225 AA. AAB98502; 

03-AUG-2001 (first entry)

Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.

Human, TADG-15, cytostatic; vaccine; ovarian tumour; cancer; tumour antigen-derived gene 15; serine protease; Stratum Corneum Chymotryptic Enzyme; SCCE.

Homo sapiens.

WO200129056-A1.

26-APR-2001.

20-OCT-2000; 2000WO-US029095.

```
Novel extracellular serine protease, termed tumor antigen-derived gene 15 protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast, ovarian cancer.
                                                                                                                      Example 10; Fig 1; 130pp; English.
                                              Tanimoto H;
                          (UYAR-) UNIV ARKANSAS.
                                                               WPI; 2001-381031/40.
                                            O'brien TJ,
```

The present invention relates to human tumour antigen-derived gene 15 (TADG-15) protein and coding sequence (see AAH23601 and AAB98500). TADG-15 is an extracellular serine protease. It was found that TADG-15 is over-expressed in overlan tumours. TADG-15 protein or its fragments of 9.20 residues that lack TADG-15 protease activity are useful for vaccinating an individual against TADG-15, having, suspected of having or at risk of getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic or therapeutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TADG-15 ; 0 100.0%; Score 47; DB 4; Length 225; 100.0%; Pred. No. 2.2; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100... Seguence 225 AA;

30 VLVNERWVL 38 1 VLVNERWVL 9 ò g

ADA05742 standard; protein; 247 AA. Human NOV18f protein SEQ ID NO:102. 06-NOV-2003 (first entry) ADA05742; 

human; NOVX; antidiabetic; anorectic; antibacterial; virucide; aimmunomodulator; cytostatic; nootropic; neuroproecetive; aimtiparKinsonian; antilparKinsonian; antilparKinsonian; antilparKinsonian; antilparKinsonian; antiparKinsonian; antiparKinsonian; alabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimar's disease; ParKinson's disease; immune disorder; haematopoletic disorder; dyplipidaemia.

Homo sapiens.

WO2003029424-AZ.

02-OCT-2002; 2002WO-US031373. 10-APR-2003

2001US-0326483P. 2001US-0327435P. 2001US-0327449P. 2001US-0327917P. 02-OCT-2001; 05-OCT-2001; 09-OCT-2001;

2001US-0328029P. 2001US-0328044P. 2001US-0328056P. 2001US-0328849P. 2001US-0329414P. 2001US-0330142P. 2001US-0330309P. 2001US-0341058P. 17-OCT-2001; 18-OCT-2001; 22-OCT-2001; 09-OCT-2001; 09-OCT-2001; 12-OCT-2001;

present invention.

24-0CT-2001; 2001US-0343629P.
29-0CT-2001; 2001US-0349575P.
01-NOV-2001; 2001US-0349575P.
17-APR-2002; 2002US-0373260P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373817P.
16-MAY-2002; 2002US-038103P.
16-MAY-2002; 2002US-038103P.
11-MAY-2002; 2002US-0381042P.
11-MAY-2002; 2002US-0381642P.
29-MAY-2002; 2002US-0381642P.
29-MAY-2002; 2002US-0381642P.
29-MAY-2002; 2002US-0381642P.
29-MAY-2002; 2002US-0381848P.
29-MAY-2002; 2002US-0381848P.
29-MAY-2002; 2002US-0381848P.
20-UNS-0202; 2002US-0383831P. 

## (CURA-) CURAGEN CORP.

thson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, curajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterron E; M, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; kets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; en AJ, Gangolli EA, Rieger DK, Spaderna SK; Patturajan M, Shimkets RA, Smithson G, Eisen AJ, Ji W,

WPI; 2003-381626/36. N-PSDB; ADA05741.

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

# Claim 1; Page 172; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising in one or more
containers, the composition described above; (3) an isolated nucleic acid
containers, the composition described above; (3) an isolated nucleic acid
comprising the nucleic acid molecule described above; (5) a call
comprising the above vector; (6) an antibody that immunospecifically
comprising the above vector (6) an antibody that immunospecifically
comprising the above polypeptide or nucleic acid molecule in
sample; (8) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a
disease associated with altered levels of expression of the above;
compression of the above polypeptide or nucleic acid molecule in a
disease associated with altered levels of expression of the above;
compression of the above polypeptide or nucleic agent for a
paver; (10) a method for identifying a potential therapeutic agent for
aberrant physpiological interactions of the polypeptide; (11) a method of
compression of activity or of latency or predisposition to
a pathology associated with the polypeptide; (12) a method for in a
correctivity of the polypeptide described above; (13) methods of traating
the activity of the polypeptide described above; (13) method of
compression of a calivities, and can be used in gene therapy. The
compression of the polypeptide and can be used in gene therapy. The
polypeptide is useful in manufacturing a medicament for treating a
colypeptide is useful in manufacturing a
colypeptide is useful in appropriation or prevent metabolic
colypeptide is useful in appropriation and colypeptide
colypeptide is useful in appropriation or prevent metabolic
colypeptide is use disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the

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immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obseity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo K, Patturajan M, Spyeek KA, Edinger SR, Ellerman K, Malyankar UM; Octt T. Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CBA, Shenoy SG;
                                                                                                                                 Gaps
                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                             100.0%; Score 47; DB 6; Length 247; 100.0%; Pred. No. 2.5; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           ADA05732 standard; protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human NOV18a protein SEQ ID NO:92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-2001; 20010S-03280445.
12-OCT-2001; 20010S-03280445.
15-OCT-2001; 20010S-03280445.
17-OCT-2001; 20010S-0330144F.
18-OCT-2001; 20010S-03303099.
24-OCT-2001; 20010S-034058.
24-OCT-2001; 20010S-034058.
25-OCT-2001; 20010S-034058.
19-APR-2002; 20010S-0340575.
19-APR-2002; 20020S-0373866.
19-APR-2002; 20020S-0373866.
19-APR-2002; 20020S-0373866.
19-APR-2002; 20020S-0373878.
16-MAY-2002; 2002US-0349779.
16-MAY-2002; 2002US-0349779.
16-MAY-2002; 2002US-0349779.
16-MAY-2002; 2002US-0349779.
17-MAY-2002; 2002US-0341038.
17-MAY-2002; 2002US-0341038.
17-MAY-2002; 2002US-0341642.
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2001US-0327449P.
2001US-0327917P.
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                         Query Match
Best Local Similarity luv...
3; Conservative
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                                                                                                                                                                                           1 VLVNERWVL 9
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Sequence 247 AA;
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The present invention describes NoVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit composition or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cellolic comprising the nucleic acid molecule described above; (5) a cellolic presence or amount of the above polypeptide cor nucleic acid molecule in a disease associated with altered levels of expression of the above and sease associated with altered levels of expression of the above a disease associated with altered levels of expression of the above and polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for abore; (10) a method for identifying a potential therapeutic agent for abore; (10) a method for identifying a pathology that is related to an aberrant expression or aberrant physological interactions of the polypeptide; (11) a method of series and adulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulation or preventing a pathology associated with the above polypeptide. Novy sequences have anitalabetic, anorectic, antipatecrally, virucide, immunomodulator, cytostatic, noorectic, antipatecrally, virucide, and antilipaemic activities, and can be used in gene therapy The coll man be used in gene therapy. The animulation associated with a human disease. The polypeptide or the nucleic syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, careary, cancer, disorders such as diabetes or obesity, infections, careary, and pathology according a pathology per
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                                                                                                                                    New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
Berghs C, Dipippo VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Shimkets RA, Rothenberg ME, Leach MD, Agee ML,
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                   Claim 1; Page 169~170; 586pp; English.
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                                                                   WPI; 2003-381626/36.
N-PSDB; ADA05731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention.
                                                                                                                                                                                                                     pharmacogenomics.
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  2 × 5 × 5 × 5 × 5 × 5
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neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia. 2001US - 0328029F 2001US - 0328044F 2001US - 0328044F 2001US - 0328049F 2001US - 0328414F 2001US - 0330142F 2001US - 0330142F 2001US - 0341058F 2001US - 0348575F 2001US - 0348575F 2001US - 0348575F 2002US - 0373815F 2002US - 0373815F 2002US-0373884P. 2002US-0374977P. 2002US-0381037P. 2002US-0381038P. 2002US-0381642P. 2002US-0383656P. 2002US-0383831P. 01-OCT-2002; 2002US-00262511. 02-OCT-2002; 2002WO-US031373 WPI; 2003-381626/36. WO2003029424-A2. Homo sapiens. -APR-2002; 19-APR-2002; 29-MAY-2002; Shimkets RA, Eisen AJ, G 

# (CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rochamberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

N-PSDB; ADA05733.

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenemics.

Claim 1, Page 170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (3) a call ocomprising the above vector; (6) an antihody that immunospecifically binds to the polypeptide described above; (7) methods for determining the parsence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the parsence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a

method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a mediulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide. Now mammal, and (14) a method for producing the above polypeptide. Now sequences have antidiabetic, anorectic, antibacterial, virucide, and antilipaemic activities, and can be used in gene therapy. The colypeptide is useful in manufacturing a medicament for treating a manifacturing a medicament for treating a cydymorphide is useful in manufacturing a medicament for treating a cid molecule may be used to disapte or the polypeptide or the nucleic acid molecule may be used to disabete or observe, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders such as Alzheimer's disease or Parkinson's probes, in chromosome mapping, tissue typing, preventual a muman NoVX from the pharmacogenomics. The present sequence represents a human NoVX from the present invention. 

Sequence 252 AA;

0; Gaps / Match Local Similarity 100.0%; Pred, No. 2.5; les 9; Conservative 0; Mismatches 0; Indels Query Match

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57 VLVNERWYL 65 1 VLVNERWVL 9 ਨੇ a

RESULT 13

AAR67888 standard; protein; 253 AA. (revised)
(first entry) 25-MAR-2003 09-AUG-1995 AAR67888; 

Human stratum corneum chymotrophic recombinant enzyme (SCCE).

Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis; callosities; keratosis pilaris; ichthyoses; eczema.

Homo sapiens

WO9500651-A1.

05-JAN-1995.

94WO-IB000166. 20-JUN-1994; 93DK-00000725. 18-JUN-1993;

(SYMB-) SYMBICOM AB.

Egelrud T, Hansson L;

WPI; 1995-052088/07. N-PSDB; AAQ81203. Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of specific inhibitors:

Disclosure; Page 97; 137pp; English.

The enzyme encoded by this sequence is used in pharmaceutical, cosmetic

SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.

08-FEB-2002; 2002WO-IBG01300. 09-FEB-2001; 2001CA-02332655. 09-FEB-2001; 2001DK-00000218.

WO200262135-AZ. Homo sapiens.

15-AUG-2002.

Human SCCE protein N-terminal fragment SEQ ID 48.

08-NOV-2002 (first entry)

ABB84421;

ABB84421 standard; peptide; 253 AA.

ABB84421 ID

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Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. B. coli) or eukaryotic (partic. AV-120 host cells. It is used to devalop products for the design and testing of cpds. useful for treating or preventing conditions associated with beta-amyloid peptide, esp. Alzheimer's disease
and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkeratotic conditions (e.g. callosities or keratosis pilaris), ichthyoses, psoriasis, eczema, etc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid pssor. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human amyloid precursor protein protease.
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Best Local Similarity luv..
Best Socal Similarity
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                                                                                                                                                                                                                                                            Sequence 253 AA;
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AAMOS383

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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence coding for a tleated within its genome, a heterologous nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous soce or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve to riss study of disease with the aim of improving treatment, to relieve cornemalized a pathogenic condition, for development or resting of a cosmetic or a pharmaceutical formulation, and for the development of a cosmetic or a pharmaceutical formulation, and for the development of a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of inflammatory skin diseases selected from diseases consisting of epidermal hyperkeratosis. The mammal of the invention is also useful the engagent of the funan stratum corneum chymotryptic enzyme, SCCE transgenic mammals described in the invention

Transgenic mammals described in the invention
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100.0%; Score 47; DB 2; Length 253; 100.0%; Pred. No. 2.5; cive 0; Mismatches 0; Indels

9; Conservative

Matches

Query Match Best Local Similarity

Sequence 253 AA;

58 VLVNERWYL 66

1 VLVNERWVL 9

Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.

Egelrud T, Hansson L;

(EGEL/) EGELRUD T. (HANS/) HANSSON L.

WPI; 2002-643380/69.

Example 6; Page 37; 74pp; English.

58 VLVNERWYL 66

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Claim 10; Page 58-59; 74pp; English. ABB84406 standard; protein; 253 AA. 08-FEB-2002; 2002WO-IB001300. 09-FEB-2001; 2001CA-02332655. 09-FEB-2001; 2001DK-00000218. 08-NOV-2002 (first entry) Egelrud T, Hansson L; WPI; 2002-643380/69. Human SCCE protein. (EGEL/) EGELRUD T. (HANS/) HANSSON L. N-PSDB; ABQ76226 Seguence 253 AA; WO200262135-A2. Homo sapiens. 15-AUG-2002. ABB84406; RESULT 14 

This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence conding for a tratum corneum chymotryptic enzyme (SCCE) or its variant, oding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, or tratum corneum chymotryptic enzyme (SCCE) or its variant, or tratum corneum chymotryptic enzyme (SCCE) or its variant, or tratum corneum chymotryptic enzyme (SCCE) or its variant, or tratument, in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or teatment of a commetic or a pharmaceutical formulation, and for the development of a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an amedal for further studies of ich mechanisms and the testing of spidermal hyperkeratosis. The mammal of the invention is also useful sea a component. This sequence represents the human stratum corneum chymotryptic enzyme, SCCE which is a serine procease synonymous with human kallikzein 7 (KLK7) and is used in the development of the invention of the corner of the invention of t Transgenic mammal or its embryo useful as model for human disease, has neterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin. SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.

Match 100.0%; Score 47; DB 5; Length 253; Local Similarity 100.0%; Pred. No. 2.5; es 9; Conservative 0; Mismatches 0; Indels Query Match Matches

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58 VLVNERWYL 66
1 VLVNERWVL 9
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Human, protease, cancer, immune-related disorder, cardiovascular disease, neuronal-associated disease; metabolic disorder; inflammatory disorder; nervos system disorder, sexual dysfunction, pain, mood disorder; hypertension, psychotic disorder; neurological disorder; dyskinesia, viral infection; human immunodeficiency virus; HIV; non-viral infection;
                                                    Amino acid sequence of novel human protease #39.
                                                                                                          ocular disease; cytostatic; enzyme.
      AAU82740 standard; protein; 253 AA.
                                    23-APR-2002 (first entry)
                     AAU82740;
AAU827
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Homo sapiens.

WO200200860-A2.

03-JAN-2002.

26-JUN-2001; 2001WO-US020171.

26-JUN-2000; 2000US-0214047P.

(SUGE-) SUGEN INC.

Whyte D, Sudarsanam S, Manning G, Caenepeel S;

WPI; 2002-139913/18. N-PSDB; ABK31782

Charydczak G;

Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory

Claim 6; Fig 2N; 313pp; English.

The present invention relates to the isolation of novel human proteases, and the mucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal-associated diseases, metabolic coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. diabetes, pain, sexual dysfunction, mood disorders, attention disorders, pain, sexual dysfunction, mood disorders, attention disorders, hypotension, hypertension, psychotic disorders, neurological disorders (e.g. Alzhahmer's disease, Parkinson's cisease) and dyskinssias. The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. human proteases of the invention

Sequence 253 AA;

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Gaps
                                               ;
0
/ Match 100.0%; Score 47; DB 5; Length 253; Local Similarity 100.0%; Pred. No. 2.5; loss 9; Conservative 0; Mismatches 0; Indels
       Query Match
                                                 Matches
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1 VLVNERWVL 9

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0; Gaps

sarch completed: March 1, 2004, 17:28:51
bb time : 47.5556 secs

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March 1, 2004, 17:35:01 ; Search time 24.1111 Seconds (without alignments) 78.818 Million cell updates/sec
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1: \( \cap \) \(\cap \) \( \cap \) \(
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                          protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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rfect score:
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Pred. No. is the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 30, Appl Sequence 49, Appl Sequence 40, Appl Sequence 50, Appl Sequence 57, Appl Sequence 5, Appl Sequence 6, Appl Sequence 6, Appl Sequence 7, Appl Sequence 8,
SUMMARIES	US-09-918-243-34 US-09-905-083-34 US-09-764-762-3 US-10-264-283-90 US-10-26-283-90 US-10-27-99-48 US-09-918-243-40 US-09-918-243-40 US-09-905-083-40 US-09-905-083-50 US-10-202-675-6 US-10-10-48-357A-7 US-10-045-357A-7 US-10-045-357A-7 US-10-045-357A-7 US-09-796-294-8
DB	- 400 000 000 000 000 000 000 000 000 00
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Score	   444444444444444   177777
Result No.	44444444444444444444444444444444444444

Sequence 34, Application US/09905083; Parent No. US20020146708A1; GENERAL INFORMATION:

RESULT 2 US-09-905-083-34

1 VLVNERWYL 9

Sequence 8, Appli	nω	'n				Ä	8	ø	H	러	ч	ч	н	ä	ř	ř	ŭ	ä	ä	ä	Seguence 194, App	ř	ä	H	equence 13	H	Sequence 194, App	Sequence 194, App
4 US-10-461-787	0 US-10-369-493-9 4 US-10-267-219-6	5 US-10-156-214,	US-09-755	US-09-755-01	4 US-10-267-219-	US-09-888	US-10-114-1	1-325-7	US-09-946-3	0-006-856A	US-10-006-818A-	US-10-01-393A	US-10-015-8	0-012-1	-006-116A-	0-006-117A-19	US-10-017-527A-	US-10-013-5	1-000-0	US-10-013-4	US-10-011-6	US-10-012-7	US-10-015-386A-	US-10-290-058A-1	US-10-011-692A-1	US-10-006-768A	-10-017-610A-	4 US-10-006-063A-194
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10	18	19	20	21	22	. 53	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

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Sequence 34, Application US/09918243
; Sequence 34, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
    APPLICANT: O'STIEN, Timothy J.
    APPLICANT: Cannon, Martin J.
    APPLICANT: Santin, Alessandro
    TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
    FILE REFERENCE: D6223CIP/CD/CIP
    CURRENT APPLICATION NUMBER: US/09/918,243
    CURRENT FILING DATE: 2001-07-30
    PRIOR FILING DATE: 2001-07-13
    FROR FILING DATE: 2001-07-13
    NUMBER OF SEQ ID NOS: 136
    SEQ ID NO 34

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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OTHER INFORMATION: Residues 58-66 of the SCCE protein
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100.0%; Score 47; DB 9; Lv
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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PPLICANT: O'Brien, Timothy J.

ITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TILE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TILE REFERENCE: D6223CIP/C/Div
URRENT APPLICATION UNDERS: US/09/905,083
PRIOR APPLICATION UNMERS: US/09/905,083
PRIOR APPLICATION UNMERS: US/09/905,000
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 47; DB 9; Length 9; Best Local Similarity 100.0%; Pred. No. 7.1e+05; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CHAIN
OTHER INFORMATION: Residues 58-66 of the SCCE protein
09-905-083-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09764762
Patent No. US20020068941A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
ITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: S
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 3174 POXTER Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parent No. USZONZONG 485615
Patent No. USZONZONG 485611
GENERAL INFORMAN, GREGORY
APPLICANT: PLOWANN, GREGORY
APPLICANT: CHARPEEL, SAN
APPLICANT: SUDARBARD
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: Z001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
SOFTWARE: PAROR FILING DATE: Z000-06-26
NUMBER OF SEQ ID NOS: 150
SSOFTWARE: PARORIT NOS: 2.1
ENGUTH SES
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Best Local Similarity 100.0
Matches 9; Conservative
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US-09-888-615-98
                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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US-09-764-762-3
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US-10-264-283-90

Sequence 90, Application US/10264283

Sequence 90, Application US/10264283

Publication No. US20303144494A1

SEPERATION No. US20303144494A1

APPLICANT: Algare, Paul A.

APPLICANT: Algare, Paul A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.590

CURRENT FILING DATE: 2002-10-02

WUMBER OF SEQ ID NOS: 111

SOFTWARE: COLIXA INVENTION DISCIOSURE Database

SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels C
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Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
CPERATING SYSTEM: DOS
SOFTWARE: FRABLEDC for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
TILING DATE: 16-7a-2001
CLASSIFICATION NUMBER: US/09/764,762
FILING DATE: 16-7a-2001
CLASSIFICATION NUMBER: US/09/764,762
FILING DATE: CLASTON:
APPLICATION NUMBER: 09/210,084
FILING DATE: CLUCKTON:
APPLICATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION INFORMATION:
TELERONE: 415-85-055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE GRARACTERISTICS:
ITELERONE: 415-85-016
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE GRARACTERISTICS:
ITENTION FOR SEQ ID NO: 3:
SEQUENCE GRARACTERISTICS:
ITENTION OF SEQ ID NO: 3:
TYPE: MAIND ACID
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TOPOLOGY: linear
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LIBRARY: GenBank
CITY: Palo Alto
                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S8 VLVNERWVL 66
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), ORGANISM: Homo sapiens
US-10-264-283-90
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                                                                             ZIP: 94304
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US-10-173-999-48
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US-09-918-243-50
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                                                                                                                                                                                                                  PEDICANT: Aziz, Matsaha
PEDICANT: Aziz, Matsaha
PEDICANT: Ginsberg, Wendy M.
PEDICANT: Ginsberg, Wendy M.
PEDICANT: Gish, Kut C.
PEDICANT: Gish, Kut C.
PEDICANT: Hevezi, Peter A.
PAPLICANT: Mack, David H.
APPLICANT: Matson, Susan R.
APPLICANT: Matson, Susan R.
APPLICANT: Ros Biotechnology, Inc.
APPLICANT: Ros Biotechnology, Inc.
APPLICANT: Ros Biotechnology, Inc.
APPLICANT: Ros Biotechnology, Inc.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Bos Biotechnology, Inc.
APPLICANT: Watson, Susan R.
APPLICANT: Bos Biotechnology, Inc.
APPLICANT: Watson, Susan R.
APPLICA
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APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Gish, Kurt C.
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
TITLE REFERENCE: 018501-002420US
CURRENT APPLICATION WUMBER: US,10,10,173,999
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION WUMBER: US 60,299,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
                                                                       quence 498, Application US/10295027
blication No. US20030232350A1
NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-10-173-999-48
Sequence 48, Application US/10173999
Publication No. US20040005563A1
GENERAL INFORMATION:
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US-10-295-027-498
                                                                                                                                                                                            PPLICANT: Afar, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 VLVNERWYL 66
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LT 6
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PRIOR FILENCE DATE: 2010-6-10.

PRIOR PRIOR DATE: 2010-6-27.

PRIOR PRIOR DATE: 2010-6-27.

PRIOR PRIOR DATE: 2010-6-27.

PRIOR PRIOR DATE: 2010-6-27.

PRIOR PRIOR PRIOR DATE: 2011-6-27.

PRIOR PRIOR PRIOR DATE: 2011-6-12.

PRIOR PRIO
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Best Local Similarity 100.0%; Pred. No. 7.1e+05; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VLVNERWVL 9
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                                                                           2 LVNERWYL 9
                                                                                                                 1 LVNERWYL 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: COMPOSITIONS CONTINUED COURSENT APPLICATION NUMBER: US/09/905,083
CURRENT APPLICATION NUMBER: US/09/905,083
PRIOR APPLICATION NUMBER: US/09/905,080
PRIOR APPLICATION NUMBER: 2001-07-13
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: O'BRIEN, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: OVATIAN Cancer
FILE REPERENCE: D6223CIP/Chiv
CURRENT APPLICATION NUMBER: U5/09/905,083
CURRENT PILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: U5/09/905,600
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 50
                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                            Nuery Match 91.5%; Score 43; DB 9; Length 9; set Local Similarity 100.0%; Pred. No. 7.18+05; atches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Match 91.5%; Score 43; DB 9; Length 9; Local Similarity 100.0%; Pred. No. 7.1e+05; les 8; Conservative 0; Mismatches 0; Indels
                                                                                         NAME/KEY: CHAIN
OTHER INFORMATION: Residues 59-67 of the SCCE protein
09-918-243-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: CHAIN
) OTHER INFORMATION: Residues 57-65 of the SCCE protein US-09-905-083-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: CHAIN

' OTHER INFORMATION: Residues 59-67 of the SCCE protein US-05-905-083-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-09-068-083-50
US-09-906-083-50
; Sequence 50, Application US/09905083
; Patent No. US20020146708A1
; Patent No. MS20020146708A1
; GENBRAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -.09-905-083-40
Sequence 40, Application US/09905083
Patent No. US20020146708A1
PERNENAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                    TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                     2 LUNERWYL 9
                                                                                                                                                                                                                                                                                                                                             1 LVNERWYL 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
  LENGTH: 9
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91.5%; Score 43; DB 9; Length 9;

Query Match

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MESUL: Application US/10202676
Sequence 6, Application US/10202676
Publication No. US20030092620A1
GENERAL INFORMATION:
APPLICANT: Lucas, John
APPLICANT: Briggs, Kristen
TITLE OF INVENTION: USE OF ADDREIN/COMPLEMENT FACTOR D IN THE TREATMENT OF METABOLIC
TITLE OF INVENTION: RELATED DISORDERS
FILE REFRENCE: 121.US2.REG
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/308,147
PRIOR PLILING DATE: 2001-07-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 228
   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 88.9%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7. Application US/10045367A

Sublication No. US20020165152A1

Publication No. US20020165152A1

GENERAL INFORMATION:

APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 14089, A NOVEL HUMAN TRYPSIN SERINE
TITLE OF INVENTION: PROTESE AND USES THERSOF

TITLE OF INVENTION: PROTESE AND USES THERSOF

CURRENT APPLICATION NUMBER: US/10/045,367A

CURRENT FILING DATE: 2002-04-15

PRIOR APPLICATION NUMBER: 60/246,561

PRIOR FILING DATE: 2000-11-07

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PASELSEQ for Windows Version 4.0

SEQ ID NO 7

LENOTH 81

TENOTH 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MANE/KEY: VARIANT
LOCATION: 27
OTHER INFORMATION: Polymorphic amino acid Ala or Gly
OTHER INFORMATION: OF THE COCATION: 34
FEATURE: INFORMATION: Polymorphic amino acid Arg or Gln
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT
100CATION: 125
OTHER TRICORMATION: Polymorphic amino acid Val or Leu
US-10-202-676-6
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APPLICANT: Rachel E. Meyers
APPLICANT: Clandt, Peter J.
APPLICANT: Curitis, Rocy A. J.
APPLICANT: Williamcon, Mark
APPLICANT: Williamcon, Mark
APPLICANT: Williamcon, Mark
APPLICANT: Williamcon, Mark
APPLICANT: Weich, Nadine
TITLE OF INVENTION: AND PROTEASE FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: 1048-191001
CURRENT PELLOGA DATE: 2002-06-13
PRIOR PELLOGATION NUMBER: US 09/797,039
PRIOR PELLOGATION NUMBER: US 09/797,039
PRIOR PILLING DATE: 2001-02-28
PRIOR PILLING DATE: 2001-02-28
PRIOR PILLING DATE: 2000-02-29
PRIOR PILLING DATE: 2000-06-15
PRIOR PILLING DATE: 2001-06-15
PRIOR PILLING DATE: 2001-06-15
PRIOR PILLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 09/934,406
PRIOR PILLING DATE: 2001-06-15
PRIOR PILLING DATE: 2001-08-21
               80.9%; Score 38; DB 13; Length 81; 75.0%; Pred. No. 32; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 99/864,801
PRIOR APPLICATION NUMBER: US 90/864,801
PRIOR FILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-19
PRIOR FILING DATE: 2001-05-19
PRIOR PLING DATE: 2000-05-19
PRIOR PLING DATE: 2001-03-06
PRIOR PLING DATE: 2001-03-06
PRIOR PLING DATE: 2001-03-05
PRIOR PLING DATE: 2001-03-05
PRIOR PLING DATE: 2001-03-05
PRIOR PLING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/187,454
PRIOR PLING DATE: 2001-03-07
PRIOR PLING DATE: 2001-03-07
PRIOR PLING DATE: 2001-03-07
PRIOR PLING DATE: 2001-04-10
PRIOR PLING DATE: 2001-04-12
PRIOR PLING DATE: 2001-04-12
PRIOR PLING DATE: 2001-04-12
PRIOR PLING DATE: 2001-04-12
PRIOR PLING DATE: 2001-03-24
PRIOR PLING DATE: 2001-03-24
PRIOR PLING DATE: 2001-03-25
PRIOR PLING DATE: 2000-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quence 57, Application US/10170789 ublication No. US20030180930A1 UNFORMATION:
ry Match
t Local Similarity 75.0°
thes 6; Conservative
                                                                                                                                                                                                                                                                                            5 LINEOWVL 12
                                                                                                                                                                                                         2 LUNERWYL 9
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0-170-789-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Amino acid sequence of mouse neuropsin homologous OTHER INFORMATION: to TADG-14; accession no. D30785
                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                         Query Match

80.9%; Score 38; DB 14; Length 81;

Best Local Similarity 75.0%; Pred. No. 32;

Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: O'Erien, Timothy J.
APPLICANT: Underwood, Lowell J.
TILE OF INVENTION: Extracellular Serine Protease
FILE REFERENCE: D6020CIP3
CURRENT APPLICATION NUMBER: US/09/796, 294
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/618,259
PRIOR APPLICATION NUMBER: US 09/618,259
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 8
PRIOR FILING DATE: 2001-03-06
PRIOR APPLICATION WIMBER: EVT/US01/07014
PRIOR FILING DATE: 2001-03-05
PRIOR PRICKATION NUMBER: US 60/187,420
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
ELENOTH: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: March 1, 2004, 18:08:50 Job time : 24.1111 secs
                                                                                                                                                                                                                                                                               ; OTHER INFORMATION; consensus sequence US-10-170-789-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 8, Application US/09796294; Patent No. US20020037581A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VLVGDRWVL 69
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ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-796-294-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. rotein - protein search, using sw model

March 1, 2004, 17:21:01 ; Search time 10.2222 Seconds (without aliqueners) (Without aliqueners/sec

US-09-905-083-34 1 VLVNERWVL 9 le: fect score:

Gapop 10.0 , Gapext 0.5 BLOSUM62 ring table:

283366 segs, 96191526 residues rched:

al number of hits satisfying chosen parameters:

nimum DB seq length: 0 ximum DB seq length: 2000000000

st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:\*
1: Dir1:\*
2: Dir2:\*
3: Dir3:\*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		serine proteinase	complement factor	tissue kallikrein	neuropsin - mouse	• •	ന	m	chymotrypsin (EC 3			hypothetical prote	serine proteinase	hypothetical prote	A21R protein - var	A22R protein - var	probable 49.1K pro	A20R protein - vac	74	pro	4	(BC	(EC 3.4	(EC 3	E E	venombin B (EC 3.4	haptoglobin Hp - c	haptoglobin Hpp -	haptoglobin - rhes	coagulation factor
	נו	A53968	рвни	KQPG	IS6559	T25594	T01779	531384	S44184	849129	T05892	F82825	A45161	T28563	C36850	C72166	T37408	D42519	T47075	T25570	S31778	831775	S49489	831776	A25852	JC2479	136945	136947	G02959	4707
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æ (	Match	100.0	83.0	ö	80.9	ö	78.7		78.7	œ	78.7	76.6							76.6								•	74.5	•	4
	Score	47	39	38	38	38	37	37	37	37	37	36	36	36	36	36	36	36	36	e M	35	35	35	35	35	3.5	35	35	35	35
	No.		N	m	4	טע	vo	7	00	Q,	10	11	12	13	14	15	16	11	18	13		21				25	26	27		59

ribosomal protein	hypothetical prote	haptoglobin precur	haptoglobin - chim		haptoglobin precur	haptoglobin - blac	нe	haptoglobin - chim	haptoglobin precur	branched-chain-ami	coagulation factor	acrosin (EC 3.4.21	hypothetical prote	unknown protein [i	probable membrane	
E70472	A83757	HPDG	136941	136942	HPHU1	900005	HPHUR	136944	HPHU2	T46034	KFBO	S11674	G96695	C86443	S54045	
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274	282	329	345	346	347	347	348	349	406	410	416	421	453	505	539	
74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	
n S	35	5	35	35	35	in m	35	32	35	35	35	35	35	35	35	
30	31	32	33	34	35	36	3.7	38	6	40	41	42	43	44	45	

### ALIGNMENTS

Asiable proteinase SCCE precursor - human
Nilternate names: stratum corneum chymotryptic enzyme
C; Species: Homo sapiens (man)
C; Species: Man)
C; Species: Man)
C; Species: Man)
C; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
R; Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J; Siol. Chem. 269, 1942e, 1994
A; Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A; Reference number: A53968; MUID:94308225; PMID:8034709
A; Reference number: A53968; MUID:94308225; PMID:8034709
A; Reference number: A53968
A; Status: preliminary
A; Molécule type: mRNA
A; Residues: 1.253 - 44A
A; Residues: 1.253 - 44A
A; Residues: GDB:377730
A; Genetics:
A; Genetics: ò 0; Gaps Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 58 VLVNERWYL 66 1 VLVNERWVL 9 RESULT 1 ઠે

RESULT 2 DBHU

Complement factor D (BC 3.4.21.46) precursor [validated] - human (fragment)

N.Alternate names: adipsin; C3 convertage activator
C5pecies: Humon sapiens (man)
C5pecies: Humon sapiens (man)
C5pecies: Humon sapiens (man)
C5pecies: Da.Aug-1985 #sequence revision 31-Dec-1992 #text\_change 08-Dec-2000
C5Accession: A40197; A60936; Ā66571; S66645
N.Mile; Numan adippin is Jancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, U.S.;
A7Ritle: Human adippin is identical to complement factor D and is expressed at high leve
A7Reference number: A40197; MulD:92250520; PMID:1374388
A7Accession: A40197; MulD:92250520; PMID:1374388
A7Accession: A40197
A7Reference number: A5.; Bennett, J.C.; Volanakis, J.E.
Biochemistry 23, 2482-2486, 1984
A7Ritle: Amino acid sequence of human D of the alternative complement pathway.
A7Reference number: A00936; MulD:85000441; PMID:6383466
A7Accession: A00936

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The state of the s
F.41,89,184/Active site: His, Asp, Ser #status experimental P:21-84,9inding site: carbohydrate (Asn) (covalent) #status experimental P:225/Binding site: carbohydrate (Asn) (covalent) #status experimental (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C'Species Caenorhabditis elegans
C'Species Caenorhabditis elegans
C'Species Caenorhabditis elegans
C'Accession: T2594
R'Sdattung. S.
A'Description: T2594
A'Status: preliminary; translated from GB/EWBL/DDBJ
A'Accession: T2594
A'Status: preliminary; translated from GB/EWBL/DDBJ
A'Rosidues: 1.417 cGAT>
A'Cross-references: EWBL:UB8308; PIDN:AAB42224.1; GSPDB:GN00019; CESP:C3228.6
A'Experimental source: strain Bristol N2; clone C3228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 80.9%; Score 38; DB 2; Length 417; Local Similarity 85.7%; Pred. No. 20; es 6; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                  Query Match
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 80.9%; Score 3%; DB 2; Length 260; Local Similarity 77.8%; Pred. No. 12; local Similarity 77.8%; Pred. No. 12; Indels 1; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Introns: 22/3; 51/2; 92/1; 297/1; 354/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         trypsin (EC 3.4.21.4) - plaice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VLVGDRWVL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 VLVNPKWVL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VLVNERWVL 9
                                                                                                                                                                                                                                                                                                                                                                        1 VLVNERWVL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 VLINERW 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VLVNERW 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene: CESP: C32E8.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuropsin - mouse
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Best Local
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issue atlikrein (EC 3.4.21.35), pancreatic - pig (tentative sequence)
issue can be corofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 24.Apt.-1984 #sequence_revision 31-Dec-1993 #text_change 31-Mar-2000
C;Accession: A00938; A92895
R;Tschesche, H; Mair, G; Godec, G; Fiedler, F; Ehret, W; Hirschauer, C; Lemon, M;
A;Tsille: The primary structure of porcine glandular kallikreins.
A;Reference number: A90015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Affolecule type: protein
Affolecule type: protein
Affolecule type: protein
Affolecule type: protein consists of two chains, A and B, held together by disulfide bonds
CfComment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release I
CfComment: Tissue kallikrein cleave Met-Lys and Arg-Ser bonds in kininogen to release I
CfComment: Tissue kallikrein bomology
Fil-224/Domain: trypsin, homology ATRY
Fil-224/Domain: trypsin homology ATRY
Fil-86/Product: tissue kallikrein chain A #status experimental <MPTA>
Fig-1-232/Product: tissue kallikrein chain B #status experimental <MPTB>
Fil-144,26-42,121-190,155-169,180-205/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             icession: $66645
Status: preliminary
Golecule type: protein
Assidues: 19-44, 'C', 46-48 cBAL>
Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, activ
Soment: Pactor D cleaves factor B when the latter is complexed with factor C3b, activ
Sometics:
Gene: GD8:DF
Cross-references: GD8:132645; OMIM:134350
Cross-references: GD8:132645; OMIM:134350
Map Dosition: Xpter-Xqter
Superfamily: trypsin; trypsin; homology
Keywords: complement alternate patterns predicted <SIG>
19-246/Product: complement factor D (fragment) #status experimental <MAT>
19-246/Product: complement factor D (fragment) #status predicted
118-141/Domain: signal sequence #status predicted cSIG>
19-246/Product: complement factor D (fragment) #status predicted
19-241/Domain: signal sequence #status predicted
19-241/Domain: signal sequence #status predicted
19-240/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                              cession: A60571
Discule type: protein
esidues: 19-20, XX', 23-27, 'XX', 30-31,'XX', 34,'X', 36-40 <MIY>
alke, N.; Holtkamp, U.; Hoerl, W.H.; Tschesche, H.
S. Lett. 371, 300-302, 1995
Title: Inhibition of degranulation of human polymorphonuclear leukocytes by complement eference number: S66645; MUID:96013156; PMID:7556615
     A.Molecule type: protein
A.Rosidues: 1-49, GML'53-134, D',136-156, H',158, B',160-224, B',226-232 <TSC>
A.Rosidues: 1-49, GML'53-134, D',136-156, H',158, B',160-224, B',226-232 <TSC>
A.Note: the residue identified as 225-Asx is bound to carbohydrate; therefore, we have it R.Bode, W.; Chen, Z.; Bartelis, K.; Kutzbach, C.; Schmidt-Kastner, G.; Bartunik, H.
J. Mol. Biol. 164, 237-282, 1983
A.Intle: Refined 2 angstrom X-ray crystal structure of porcine pancreatic kallikrein A, t. structure and its comparison with bovine trypsin.
A.Rosieference number: A92895; MUID: 83189107; PMID: 6551452
A.Coession: A92895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.0%; Score 39; DB 1; Length 246;
88.9%; Pred. No. 7.5;
trive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity bo...
Best Local Similarity
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Gaps

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Chymotrypsin (BC 3.4.21.1) 1 precursor - African malaria mosquito
NiAlternate names: chymotrypsin-like proteinase ANCHYNI
NiAlternate names: chymotrypsin-like proteinase ANCHYNI
NiAlternate names: chymotrypsin-like proteinase ANCHYNI
Cibate: 19-May-2000 #sequence (African malaria mosquito)
Cibate: 19-May-2000 #sequence (African malaria mosquito)
Cibate: 19-May-2000 #sequence revision 19-May-2000 #text_change 19-May-2000
Cibate: 19-May-2000 #sequence revision 19-May-2000 #text_change 19-May-2000
RyMueller, N.
NiMeller, N.
NiMeller, N.
NiPerciption: Cloning of blood meal induced serine protease genes of the mosquito Anoph, A;Reference number: 835412
A;Reference number: 836129
A;Reference n
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C;Species: Arabidopsis thaliana (mouse-car cress)
C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 13-Aug-1999
C;Accession: T05892
R;Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Bancroft, I.; Mewe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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A,Accession: S44185
A,Accession: S44185
A,Cross-references: EMBL,232645; NID:g474026; PIDN:CAA83568.1; PID:g474028
A,Esterinces: EMBL,232645; NID:g474026; PIDN:CAA83568.1; PID:g474028
A,Experimental source: strain Suakoko
C,Genetics:
A,Introns: 78/2; 203) trypsin homology
C,Reywords: hydrolase; procein digestion; serine proteinase
F;1-17/Domain: signal sequence #status predicted <PRO>F;18-32/Domain: activation peptide #status predicted <PRO>F;33-259/Product: chymotrypsin 1 #status predicted <PRO>F;33-250/Domain: trypsin homology <PRO>F;33
A; Cross-references: EMBL: Z18888; NID: 9509416; PIDN: CAA79326.1; PID: 9509417
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es 6; Conserv
                                                                                                                        A; Introns: 78/2; 209/3
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Chymotrypsin (EC 3.4.21.1) 2 precursor - African malaria mosquito

Chymotrypsin (EC 3.4.21.1) 2 precursor - African malaria

Chymotrypsin (EC 3.4.21.1) 2 precursor - African malaria

Chymotrypsin (BC 3.4.21.1)

Chymotrypsin (African malaria mosquito)

Chymotry 2000 #sequence_revision 19-May-2000 #text_change 19-May-2000

Chymotler, H.M.; Catteruccha, F.; Crisanti, A.

Submitted to the EMED Data Library, April 1994

Alpescription: An Amopheles gambiae locus containing the sequences of two closely relate

A.Reference number: S44184

A.Molecule type: DNA

A.Molecule type: DNA

A.Molecule type: DNA
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submitted to the EMBL Data Library, November 1992
submitted to the EMBL Data Library, November 1992
A; Reference number: S35412
A; Reference number: S35412
A; Accession: S49130
A; Molecule Lype: DNA
A; Restadues 1-165, 'R', 167-193,' FPD', 197-258 <MU2>
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Typsin (EC 3.4.21.4) - plaice
;Speciaes: Pleuronectes placessa (plaice)
;Speciaes: Pleuronectes placessa (plaice)
;Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 18-Jul-1997
;Accession: 53.384
;Leaver, M.J. George, S.G.
bhmitted to the BMBL Data Library, November 1990
;Reference number: 530567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-258 <MUE>
A;Cross-references: EMBL:Z32645; NID:g474026; PIDN:CAA63567.1; PID:g474027
R;Mueller, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.7%; Score 37; DB 2; Length 250;
66.7%; Pred. No. 18;
trive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ross-references: EMBL:X56744; NID:g1213630; PID:g64240

uperfamily: trypsin, trypsin, homology

ESWORDS: hydrolass; protein digestion; serine proteinase

i3-242/Domain: trypsin homology <TRY:
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J.Supertamily: trypsin: trypsin: trypsin digestion; serine proteinase
J.Keywords: hydrolase; protein digestion; serine proteinase
F;23-242/Domain: trypsin homology <TRX>
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ses 6; Conservative
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.;Molecule type: mRNA
;;Residues: 1-250 <LEA>
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Sest Local S
Watches 6
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A; Reference number: A45161; MUID: 93077530; PMID: 1447189
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C72166
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;Simpson, A. U. G.; Relanach, F. C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Arriches, M. S.; Bueno, M.R.F.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, A. Ba-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Fernica, A.J.S.
indicted to GenBank, June 2000
A,Authors: Perreira, V.C.A.; Ferro, J.A.; Fraga, U.S.; Franca, S.C.; Franco, M.C.; Frohm A,Authors: Perreira, M.C.; Kengihan, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigt ciado, M.A.; Madeira, A.M. B.N.; Machina, C.L.; Marques, M.V.; Martins, E.A.; Matchins, E.C.; Margues, W.; Martins, E.C.; Margues, W.; Martins, E.C.; Margues, W.; Martins, E.C.; Margues, W.; Rodrigues, W.; Rosa, A.U. de M.; de Oliveira, M.C.; de Sa, R.G.; Santelli, R.V.; Sawasak A,Authors: da Silva, A. A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Silva Jr., M.A.; da Silva, A.M.; Almeida, S.; Vettore, A.L.; Z.M., A.M.; Silva Jr., M.A.; da Silva, A.M.; Silva Jr., M.A.; M.A.; da Silva, A.M.; Silva Jr., M.A.; M.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine proteinase (EC 3.4.21.-) RNK-Met-1 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Daceise: Rattus norvegicus (Norway rat)
C;Date: 2-may-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C;Accession: A45161
R;Smyth, M.J; Wilrrout, T.; Trapani, J.A.; Ottaway, K.S.; Sowder, R.; Henderson, L.E.; J. Biol. Chem. 267, 24418-24425, 1992
A,Puttle Purification and cloning of a novel serine protease, RNK-Met-1, from the granul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pochetical protein XF0279 [imported] - Xylella fastidiosa (strain 9a5c)
Species: Xylella fastidiosa
Date: Xylella fastidiosa
Date: Repair: Reference revision 20-Aug-2000 #text_change 20-Aug-2000
Accession: Ref282:
Ranonymous. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Fittle: The genome sequence of the plant pathogen Xylella fastidiosa.
Reference number: A62515; MUID:20365717; PMID:10910347
Reference number: A62515; Muid: See reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                       ap position: 5
Throns: 72/3; 142/3; 227/2; 344/3; 372/3; 941/2; 1016/3; 1038/3; 1055/1; 1095/2; 1155
ote: F6H11.110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.7%; Score 37; DB 2; Length 1421; 66.7%; Pred. No. 1.1e+02; tive 2; Mismatches 1; Indels
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itted to the Protein Sequence Database, April 1998 ference number: Z15456 cession: T05892 incure type: DA Sequence Total Cabo. Sidues: 1-1421 cabo. Sidues: EMBL. AL021684 cost references: EMBL. AL021684 sequence source: cultivar Columbia; BAC clone F6H11 shetics:
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;Molecule type: DNA
;Residues: 1-72 <SIM>
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hypothetical protein A21R - variola major virus
Cypecides; variola major virus
Cypecidesion: T28563
AyTitle: Potential virulence determinants in terminal regions of variola smallpox virus syletteence number: Z20488; MUID:9408847; PMID:8264798
AyTitle: Potential virulence determinants in terminal regions of variola smallpox virus sylecession: T28563
AyRocession: T28563
AyRocession: T28563
AyRolecule type: DNA
AyRosidues: 1-426 - AMS>
Cyperimental source: strain Bangladesh-1975
Cysperfamily: vaccinia virus probable 49.1K protein
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C;Date: 30-6ep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C;Accession: C36850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyacession. C36850

Explinov, V.M.

Submitted to GenBank, November 1992

A;Reference number: A36859

A;Reference number: A36859

A;Reference number: B8859

A;Molecule type: DNA

A;References: Dreliminary

A;Rolecule type: DNA

A;Cross-references: GB:X69198; NID:g456758; PIDN:CAA49065.1; PID:g297303

C;Superfamily: vaccinia virus probable 49.1K protein
A;Accession: A45:51
A;Saccession: A45:51
A;Restdues: pre-liminary
A;Restdues: 1-258 <SWX>
A;Restdues: 1-258 <SWX>
A;Cesdances: GBLU5175; NID:g206691; PIDN:AAA42056.1; PID:g206692
C;Superfamily: trypsin homology
C;Keywords: hydrolase; serine proteinase
F;21-245/Domain: trypsin homology <TRX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.6%; Score 36; DB 2; Length 426; 55.6%; Pred. No. 49; ative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7%; Pred. No. 29; Length 258;
Matches 6; Conservative 3; Mismatches 0; Indels
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0; Gaps

yarch completed: March 1, 2004, 17:36:28
yb time : 10.3333 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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March 1, 2004, 17:20:41; Search time 30.3333 Seconds (without alignments) 93.615 Million cell updates/sec US-09-905-083-34 tle: rfect score: quence:

1 VLVNERWVL 9 oring table:

1017041 seqs, 315518202 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 arched:

1017041 tal number of hits satisfying chosen parameters:

.nimum DB seq length: 0 iximum DB seq length: 20000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

stabase :

SPTREMBL\_25:\*
1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungl:\*
4: sp\_fungl:\*
5: sp\_fungl:\*
6: sp\_fungl:\*
5: sp\_fungl:\*
6: sp\_fungl: sp\_virus:\*
sp\_virus:\*
sp\_vuclassified:\*
sp\_tvirus:\*
sp\_tvirus:\*
sp\_bacteriap:\* sp plant:\* sp archeap:\* 04444444 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

									,								
	Description	Qen5n9 homo sapien	O9ffr7 arabidopsis	Q9myv8 bos taurus	Q8jfg7 gadus morhu	Q9xy58 ctenocephal	Q7sze2 agkistrodon	Q7z0g5 phlebotomus	Q8t3b8 caenorhabdi	Q9sny8 solanum tub	Q9sny9 solanum tub	P91123 caenorhabdi	Q9pt51 agkistrodon	Q8uuj1 agkistrodon	Q9vem7 drosophila	Q9w6k0 notothenia	092046 dissostichu
COLUMNICO	ΙD	QBN5N9	O9FFR7	Q9MYV8	Q8JFQ7	Q9XY58	Q7SZE2	Q7Z0G5	Q8T3B8			P91123	Q9PT51	Q8UUJ1	Q9VEM7	O9W6K0	092046
	DB	4	10	φ	13	S	13	Ŋ	Ŋ	10	10	Ŋ	13	13	ហ	13	13
	% Query Match Length DB	253	455	100	249	223	234	262	313	377	418	461	233	234	243	249	249
	% Query Match	100.0	85.1	83.0	83.0	80.9	80.9	80.9	80.9	80.9	80.9	80.9	78.7	78.7	78.7	78.7	78.7
	Score	47	04	6 E	39	38	98	38	38	38	38	38	37	37	37	37	37
	Result No.	н	7	m	4	S	9	7	80	σv	10	11	12	13	14	15	16

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0; Gaps

O93265 pseudopleur O97098 anopheles a O97100 anopheles d O9ptl3 agkietrodon Q9ygj9 agkietrodon	Q9xy53 ctenocephal Q7szel gloydius sa Q8uNk2 crotalus ad Q8mk3 crotalus at Q8mk3 crotalus at		Q9ukrz homo sapien O45648 amopheles g Q98n76 rhizobium l Q9v887 drosophila Q9ys87 rettus norv Q92ysy rettus norv		Q81193 ectromelia Q89166 variola vir Q80hv4 vaccinia vi Q80dv4 cowpox viru
13 093265 5 097098 5 097100 13 0987L3 13 098G49	5 Q9XYS3 13 Q7SZE1 13 Q8UUK2 13 Q8QHK3		00 0		12 Q8JL93 12 Q89166 12 Q80HV4 12 Q80DV4
255 255 255 257 257	22 22 22 42 42 43 43 43 43 43 43 43 43 43 43 43 43 43	348 675 1176 72	111222224 122224 122224	0 4 4 4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0	4444 6244 6246 646
78.7 78.7 78.7 78.7	7.887 7.887 7.87	78.778.7	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	76.6	76.6 76.6 76.6
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## ALIGNMENTS

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01-OCT_2002 (TrEMBLrel. 22, Created)
01-OCT_2002 (TrEMBLrel. 22, Last sequence update)
01-OCT_2003 (TrEMBLrel. 25, Last annotation update)
Kallikrein 7 (chymotryptic, stratum corneum).
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9506;
                                                                                                                                                                                                                                                                                                                                                                                 LISOLAGENER,

STRANDENER,

STRANDENER,

1. SUDMILLEG (JUN-2002) to the EMBL/GenBank/DDBJ databases.

-1 SINILLARITY: BELONGS TO PEPTIDASE FAMILY SI.

EMBL, BCO32005, AAH32005.1, -.

R GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:chymotrapsin activity; IEA.

GO; GO:0004295; F:crypsin activity; IEA.

R GO; GO:0004295; F:crypsin activity; IEA.

R GO; GO:0004295; F:crypsin activity; IEA.

R GO; GO:0004295; F:crypsin activity; IEA.

IN InterPro; IRNO0129; F:proteolypsis and peptidolysis; IEA.

R InterPro; IRNO0129; F:profidase_S1.

R FRINTS; FR00099; Lrypsin, 1.

R PROMITS; FR00090; TRYPSIN, 1.

R PROSITE; PS00134; TRYPSIN, 1.

R PROSITE; PS00134; TRYPSIN, 1.

R PROSITE; PS00135; TRYPSIN, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cuery Match
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                   253 AA.
                                                   PRT;
                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                 GNSN80
RESULT 1
                         GNSN80
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Gaps

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Length 100;

Score 39; DB 6; Pred. No. 8.2;

83.0%;

2; Mismatches

1 10 10 100 AA; 11239 MW; FFFEGAESAB43CED9 CRC64;

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PROSITE; PS50240; TRYPSIN_DOM; 1.
Hydrolase; Protease; Serine protease.
NON_TER 1 1
NON_TER 100 100
SEQÜENCE 100 AA; 11239 MW; FFFEGAI
                                                                                     Query Match
Best Local Similarity 75.v
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Q9XY58
ID Q9XY58
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MEDLINE-97411969; PubMed-9330910;
MEDLINE-97411969; PubMed-9330910;
MEDLINE-97411969; PubMed-9330910;
Miyajima N., Tabata S.;
Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence of the 1.6 Mb regions covered by twenty physically assigned pl clones."
DNA Res 4:421-230 (1997).
EMBL; AB005233; BAB114691; -.
InterPro; IPR001810; F-box.
InterPro; IPR001810; F-box.
InterPro; IPR00845; Skpl_Skp2.
Pfam; PF00646; F-box: 1.
Pfam; PF00646; F-box: 1.
Pfam; PF00646; F-box: 1.
                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-201 (TrEMBLrel. 16, Last sequence update)
01-MAR-201 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amnotation update)
Genomic DNA, chromosome 5, Pl clone:MBK23.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicocyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
MCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lavery K.S., Gabler C., Killian G.J.; "Expression and localization of haptoglobin in the bovine female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 85.1%; Score 40; DB 10; Length 455; Best Local Similarity 75.0%; Pred. No. 26; Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reproductive tract...;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ271156; CAC00531.1; -. HSSP, P00784; IBAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WEROPS; SOI.972; --
OS. GO:000823; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser trypsin.
Ferny: IPR009003; Cys Ser trypsin.
Fem; PF00089; trypsin; 1.
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Last annotation update)
                                                                                                                               455 AA
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01-0CT-2000 (TrEMBLrel. 15,
01-0CT-2003 (TrEMBLrel. 25,
Haptoglobin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 IINERWVL 111
                            58 VLVNERWYL 66
     1 VLVNERWVL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LUNERWYL 9
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                             Gadus morthua (Atlantic cod).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Ectinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spilliaert R.;

"Atlantic Cod Trypsin Y - Member of a Novel Trypsin Group.";

"Atlantic Cod Trypsin Y - Member of a Novel Trypsin Group.";

"A Similarity: BELOWGS TO PEPTIDASE FAMILY SI.

"EMBL; AJ49311; CAD30563.1; -

"EMBL; AJ49311; EA.

"A GO; GO:0006295; F:trypsin activity; IEA.

"R GO; GO:0006508; P:trypsin activity; IEA.

"R GO; GO:0006508; P:trypsin activity; IEA.

"R GO; GO:0006508; P:trypsin activity; IEA.

"EMBL; AJ49311; Peptidase ASIA.

"InterPro; IPR001254; Peptidase SIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUB-Pyloric caecum;
Gudmundsdottir A.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 AA; 27400 MW; 8FB98462CEDBEFC9 CRC64;
                                                                                                                                                                                              OBSUFG7 PRELIMINARY; PRT; 249 AA. 080FG7; 01-0CT-2002 (TEMBLrel. 22, Created) 01-0CT-2002 (TEMBLrel. 22, Last sequence update) 01-0CT-2003 (TEMBLrel. 25, Last annotation update) 17-ypsinogen Y precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00089; trypsin; 1.

PRINTS; PR00122; HTMORRYPSIN.

SMART; SW00020; Tryp SPC; 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00135; TRYPSIN SRF; 1.

Hydrolase; Protease; Serine protease; Signal.

SIGNAL
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249 249
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TISSUE=Pyloric caecum;
PubMed=10612685;
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22 LINERWLL 29
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Best Local Similarity
Matches 6; Conserv
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2 LUNERWYL
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SEQUENCE
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30 LVNEEWVL 37

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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein.
C32E8.6.
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Best Local Similarity 75...
6; Conservative
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57 ILNERWVL 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=29031;
                                                                                                                                                                                                                                                                                                                                                                           Chymotrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gattung S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBT3B8
                                                                                                                                                                                     Q7Z0G5
                                                                                              RESULT 7
Q7Z0G5
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Gaines P.J., Sampson C.M., Rushlow K.E., Stiegler G.L.,

"Cloning of a family of serine protease genes from the cat flea
"Cloning of a family of serine protease genes from the cat flea
"Cloning of a family of serine protease genes from the cat flea
"Cloning of a family of serine protease genes from the cat flea
"Insect Mol. Biol. 81:11-22(1999).

"Insect Mol. 81:11-22(1999).

R EMBLA ARD2836; Pab21836.1; -

R PRSP, POOT066: LCHG

GO; GO:0004253; Firtypsin activity; IEA.

GO; GO:0004295; Firtypsin activity; IEA.

R O; GO:0004295; Firtypsin activity; IEA.

R O; GO:0005083; Firtypsin activity; IEA.

R O; GO:0005089; Prypein activity; IEA.

R InterPro; IPR001254; Peptidase_S1A.

R InterPro; IPR001254; Peptidase_S1A.

R PRINT; SM00020; Tryp SPC; 1.

R PROSITE; PS00134; TRYPSIN HIS; 1.

R PROSITE; PS00134; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               075ZE2;
01-OCT-2003 (TERMELRE1. 25, Last sequence update)
01-OCT-2003 (TERMELRE1. 25, Last sequence update)
01-OCT-2003 (TERMELRE1. 25, Last annocation update)
Thrombin-like enzyme defibrase (Fragment).
Agkistrodon caliginosus (Korean viper) (Gloydius ussuriensis).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
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0
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chymotrypsin-like serine protease (Fragment).
SP-4.
Ctenocephalides felis (Cat flea).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Ctenocephalides.
Ctenocephalides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 80.9%; Score 38; DB 13; Length 234; Best Local Similarity 87.5%; Pred. No. 31; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.9%; Score 38; DB 5; Length 223; 75.0%; Pred. No. 29; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Venom gland;
Sun D.-J., Yang T.-S.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY204242; AAP20637.1; -.
NON TER 1
SEQUENCE 234 AA; 25351 MW; 0124C1485525F560 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 AA; 24844 MW; C34EBE9455DD7DE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase, Protease, Serine protease.
NON TER 1 1
SEQUENCE 223 AA, 24844 MW, C34EBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7515;
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Gaps

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Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                             TISSUB-MIGHT.

TISSUB-MIGHT.

TISSUB-MIGHT.

TISSUB-MIGHT.

Valenzuela J.G.;

Valenzuela J.G.;

"Cloning and characterization of trypsins and chymotrypsins-like proteases from the midgut of the sand fly vector Phlebotomus papacasi.";

Gun-2002 to the EMBL/GenBank/DDBJ databases.

Submitted (UNN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AY128106; AAMS6938.1; -.

SEQUENCE 262 AA, 28863 MW; 31F11012206A65D4 CRC64;
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                                                                                             Phlebotomus papatasi.
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopter-Ygota, Diptera, Nematocera, Psychodoidea,
Bsychodidae, Phlebotomus.
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STRAIN=Bristol N2;
Waterston R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, 1983081, AAM15557.1;
WormPep; C32E8.6b; CE30371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The sequence of C. elegans cosmid C32E8."; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases
01-07T-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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MEDLINE=99069613; PubMed=9851916;
Waterston R.;
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P91123
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P91123
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STRAIN=CV. Russet Burbank;
STRAIN=CV. Russet Burbank;
Campbell M.A., Patel J.K., Meyers J.L., Myrick L.C.;
Campbell M.A., Patel J.K., Meyers J.L., Myrick L.C.;
"Isolation of a functional gene encoding for branched-chain amino acid aminotransferase from potato.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF193846; AAR07192.1;
HSSP; P00510; 1A3G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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Solanum tuberosum (Potato).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                     Score 38; DB 5; Length 313;
Pred. No. 42;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 25, Last annotation update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Branched-chain amino acid aminotransferase (EC 2.6.1.42).
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01-MAY-2000 (TFEMBLrel. 13, Created)
01-MAY-2000 (TFEMBLrel. 13, Last sequence update)
01-CCT-2003 (TFEMBLrel. 25, Last annotation update)
Branched-chain amino acid aminotransferase (EC 2.6.1.42).
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                                                                                                                                                                                                                                                 35608 MW; 4372ED66478E434A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
GO, GO:0003824; F:catalytic activity; IEA. GO:000152; P:meteabolism; IEA.. InterPro; IPR000873; AMP-bind. Pfam; PF00501; AMP-binding; I. PR00517; AMP-binding; I. Hypochetical protein. S00485; AMP BINDING; I. Bypochetical 313 AA; 35608 MW; 4372ED66478
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                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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219 VLINERW 225
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Best Local Similarity
Matches 6, Conserva
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Best Local Similarity
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9SNY9
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GO; GO:0004084; F:branched-chain-amino-acid transaminase acti. .; IEA. GO; GO:0004084; F:branched-chain-amino-acid transaminase acti. .; IEA. GO; GO:0016740; F:transferase activity; IEA. GO; GO:0008122; P:merabolism; IEA. InterPro; IPR001544; Aminotrans IV. InterPro; IPR001544; Aminotrans IV. InterPro; IPR005786; B_amino_transII. ProDom; PD001961; Aminotrans 4; 1. TIGRRAMS; TIGRRAMS; IVE_II 1. Aminotransferase; Transferase.
                                                                               SEQUENCE FROM N.A.
STRAIN=cv. Russet Burbank;
Campbell M.A., Patel J.K., Meyers J.L., Myrick L.C.;
Campbell M.A., Patel J.K., Meyers J.L., Myrick L.C.;
"Isolation of a functional gene encoding for branched-chain amino acid aminotransferase from potato.";
Submitted (OCT.1999) to the EMBL/GenBank/DDBJ databases.
EMBL; APL93845; AAF07191.1; -.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
NCBL_TaxID=4113;
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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Pred. No. 57;
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"Direct Submission.";
"Direct GuDM-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 188308, AAB4234.2; -.
PIR; T25594; T25594.
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"The sequence of C. elegans cosmid C32E8.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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Wormbep, 0.3288.6a, CE27814.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
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MEDLINE=99069613; PubMed=9851916;
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Best Local Similarity 75.0%;
Matches 6; Conservative
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VLANERWI 195
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STRAIN-Bristol N2;
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Thrombin-like enzyme ussurase (Fragment)
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Q9VEM7
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MEDLINE=2032322; PubMed=10845699;

Lee J.W., Park W. J.

Lee J.W., Park W. J.

Lee J.W., Park W. J.

Lenzyme from Agkistrodon blomhoffil brevicaudus snake venom, by serial hybridization-polymeras echain reaction.";

Arch. Biochem. Biophys. 377:24-240(2000).

L. Arch. Biochem. Biophys. 377:24-240(2000).

REMEL, AJ24775; DAB65936.1;

RESP; PO0763; IDPO.

MEXOPS; S01.185; -..

GO; GO:0004235; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:chymotrypsin activity; IEA.

GO; GO:0006568; P:proteolysis and peptidolysis; IEA.

MILEPPO; IPRO0134; Peptidase_S1.

InterPro; IPRO01314; Peptidase_S1.

InterPro; IPRO0122; CHYMOTRYPSIN.

SWART; SMO0722; CHYMOTRYPSIN.

RESPRESSING PROSING REXPERINDEN.

RESSITE; PSO0134; TRYPSIN DOM; 1.

PROSITE; PSO0134; TRYPSIN DOM; 1.

PROSITE; PSO0134; TRYPSIN JER; 1.

PROSITE; PSO0134; TRYPSIN JER; 1.

PROSITE; PROSITE; PROSING SER; 1.

PROSITE; PROSITE
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Agkietrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).

Agkietrodon halys blomhoffi (Mamushi) (Strebrata; Buteleostomi;
Lebidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Agkistrodon.
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                                                                                                                80.9%; Score 38; DB 5; Length 461;
85.7%; Pred. No. 63;
ive 1; Mismatches 0; Indels
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    Pfam; PF00501; AMP-binding; 2.
PR051TE; P800455; AMP_BINDING; 1.
Hypothetical protein.
SEQUENCE 461 AA; 51902 MW; 8662F7486A0E57A1 CRC64;
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Beta-fibrinogenase (Fragment).
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NON TER 1
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Q8UUJ1,
01-MAR-2002 (TEMBLrel. 20,
01-MAR-2002 (TEMBLrel. 20,
01-OCT-2003 (TEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                       Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 LINEEWUL 36
                                                                                                                                                                                                                                            219 VLINERW 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 LUNERWUL 9
                                                                                                                                                                                                            1 VLVNERW 7
                                                                                                                                                                                                                                                                                                                                                                             Q9PT51
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GTRAINSEPERKEIEY;

KM MEDLINE=20196066; PubMed=10731132;

Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D. Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

A George R.A., Lewis S.E., Richards S., Abhburner M., Henderson S.N.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Ann K.H., Doyle C., Baxter E.G., Helt G., Nalson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxmanale J., Bayraktaroglu L., Beasley E.M.,

Beson K.Y., Benos P.V., Berman B.P., Blandari D., Bolahakov S.,

Borkova D., Bottchan M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
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Agkistrodon caliginosus (Korean viper) (Gloydius ussuriensis).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Epidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Poison gland;
Daolin D., Xiaodong D., Wenfang W., Anguo L., Mei X.;
Daolin D., Xiaodong D., Wenfang W., Anguo L., Mei X.;
"Cloning and Sequence Analysis of CDNAs for Thrombin-like Enzymes,
"Cloning and Sequence Analysis of CDNAs for Thrombin-like Enzymes,
USSULIN and USSULASSE, From Agkistrodon halys ussuriensis Snake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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Drosophila merazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
CG4053 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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de Pablos B., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriers S., Fleischmann W.,
Fosler C., Gabriellan A.B., Garraz C., Gelbart W.M., Glasser K.,
Altris N.L., Harvey D., Helman T.J., Hernandez J.F., Houck J.,
Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Morkulov G. Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mortus S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson K.M., Moy M., Murphy B., Nusskern D.R., Pacleb J.M.,
Rainer K., Semington K.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K.S., Pan S., Pollard J., Puri V., Reese M.G.,
Shier E., Spradling A.C., Staplecon M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Staplecon M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Staplecon M., Skupski M.P., Smith T.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho X., Smith H.O.,
A Glabs R.A., Myers B.W., Rubin G.M., Venter J.C.;
Mithe genome sequence of Drosophila melanogaster.";
C. Schence 287:2185-2195(2000).

Hand S. Mand S. M. M. Mand S. M. M. M. M. S., Zhu X., Smith H.O.,
Mith S. M. M. Rubin G.M., Venter J.C.;
Mithe S. Sidence 287:2185-2195(2000).

Hand S. M. M. S. M. M. M. S. M. M. M. S., Zhu X., Smith H.O.,
Mithe S. M. M. M. M. Rubin G.M., Venter J.C.;
Mithe S. Sidence 287:2185-2195(2000).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Trypsinogen-1ike serine protease.
Notothenia coriiceps (black rockcod).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Suteleostei; Neoteleostei; Nototheniomorpha; Acanthopperygii; Percomorpha; Perciformes; Notothenioidei; Notothenia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 5; Length 243;
Pred. No. 50;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0722; CHYMOTRYBSIN.
SMART; SMOOZO; TRYPSIN BPC; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN BSK; 1.
PROSITE; PS00135; TRYPSIN BSK; 1.
PROSITE; PS00136; TRYPSIN BSK; 1.
SEQUENCE 243 AA; 26992 MW; 393C4B710563C811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO, GO:0004263; Fichymotrypsin activity; IEA. GO; GO:0008233; Fichymotrypsin activity; IEA. GO; GO:0004295; Fitrypsin activity; IEA. GO; GO:0006509; Pitrypsin activity; IEA. GO; GO:0006509; Pitrypsin activity; IEA. InterPro; IPR00103; Cys Ser trypsin. InterPro; IPR001254; Peptidase_S1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003716; AAF55394.1; -. HSSP; P00766; 1CHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0038482; CG4053.
GO; GO:0004263; F:chymotrypsi
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Best Local Similarity 55.6%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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RI Glycoprotein captured.";

RI Nature 0:0-0(1999).

C. - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

DR HSPP; PO0761; IEPT.

DR HSSP; PO0761; IEPT.

DR GO; GO:0004235; F:CPPPIDASE activity; IEA.

DR GO; GO:0004295; F:CPPPIDASE activity; IEA.

DR GO; GO:0006233; F:CPPPIDASE activity; IEA.

DR HCAPTO; IPRO01254; Peptidase_S1.

DR INTERPO; IPRO01254; Peptidase_S1.

DR PROSITE; PS001254; Peptidase_S1A.

DR PROSITE; PS001255; TRYPSIN SER; 1.

DR PROSITE; PS001255; TRYPSIN SER; 1.

DR PROSITE; PS00155; TRYPSIN SER; 1.

Mydrolase; Portease; Serime protease.

SQ SQUENCE 249 AA; 27419 MW; 69C0B72DFB96ED6 CRC64;

Authority Actor

Query Match

QV I VLVNERWUL 9

CQ I VLNNERWUL 56

CQ I LN GO I COMPANA I, 2004, 17:34:47
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bacillus su lachesis mu agkistrodon bothrops ja

homo sapien homo sapien arabidopsis

P00738 Q9m401 P00741

homo sapien sapien bos taurus

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P10323 P09871 P45900 P33589 P09872 P81824

ateles geof

sus scrota

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Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A., Egelrud T.;
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Biochem. Biophys. Res. Commun. 211:586-589(1995).
-!- FUNCTION: May catalyze the degradation of intercellular cohesive
structures in the cornified layer of the skin in the continuous
shedding of cells from the skin surface. Specific for amino acid
residues with aromatic side chains in the Pl position. SCCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skytt A., Stroemgyist M., Egelrud T., "Primary substrate specificity of recombinant human stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
110-0CT-2003 (Rel. 42, Last annotation update)
enzymein 7 precursor (EC 3.4.21.-) (Stratum corneum chymotryptic enzyme) (hSCCE).
KLK7 OR PRSS6 OR SCCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hansson L., Backman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T.;
Papidermal oversexpression of stratum corneum chymotryptic enzyme mice; a model for chronic ithchy dermatitis ", Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE=20510030; PubMed=11054574; Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J Moss P., Paeper B., Wang K.; Sequencing and expression analysis of the serine protease gene cluster located in ohromosome 19q13 region."; Gene 257:119-130(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase."; J. Biol. Chem. 269:19420-19426(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Keratinocytes;
Yousef G.M., Scorilas A., Diamandis B.P.;
"Molecular characterization, mapping and tissue expression of human stratum corneum chymotryptic enzyme gene.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A., AND SEQUENCE OF 23-53.
                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                        HPT PIG
HPTR HUMAN
HPT HUMAN
BCA3 ARATH
FA9 BOVIN
ACRO HUMAN
                                                                                                                                               ACRO HUMAN
C1S HUMAN
YOAC BACSU
VSPA LACMU
VSP1 AGKCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94308225; PubMed=8034709;
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MEDLINE=95314630; PubMed=7794273;
                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Human)
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NCBI_TaxID=9606;
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SEQUENCE
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P49862:
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KLK7
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091511 trimeresuru
094694 trimeresuru
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                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-1-Tyr-26, and 26-Tyr-|-The-7). Could play a role in the activation of precursors to inflammatory cytokines.

TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Very low levels are also seen in the brain and kidney.

SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
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GO; GO: 000844; P: epidermal differentiation; TAS.

InterPro; IPR009003; Cys_Ser_trypsin.

InterPro; IPR001314; Peptidase_S1A.

InterPro; IPR001314; Peptidase_S1A.

Fram; PR00189; trypsin; 1.

FRINT; PR00722; CTYMOTRYPSIN.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00134; TRYPSIN BIS; 1.
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2D68B6B15A76A668 CRC64;
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EMBL, AF166330, AAD4918.1, --
EMBL, AF43527, AAG33360.1, --
EMBL, AF332583, AAK69624.1, --
PIR, A53968, A53968, AS3968, MESCPS, BOOTG3, BDPO.
MERCPS, SO1.300, --
Genew, HGNC 6368, KLK7.
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 42, Last annotation update)
Glandular kallikrein precursor (EC 3.4.21.35) (Tissue kallikrein).
Sus scrofa (Pig)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI\_TAXID=9823;

246 AA

PRT;

STANDARD;

KLK PIG P00752;

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"Refined 2-A X-ray crystal structure of porcine pancreatic kallikrein A, a specific trypsin-like serine proteinase. Crystallization, structure determination, crystalliographic refinement, structure and lits comparison with bowine trypsin."; J. Mol. Biol. 164:237-282(1963).
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                                                                                     "Generation of alpha- and beta-kallikreins from porcine pancreatic prokallikrein by the action of trypsin."; Chem. Pharm. Bull, 36:4891-4899(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE=90336040; PubMed=2379280; Kamada M., Kizuki K., Moriya H., Kamada M., Ikekita M., Kurahashi T., Aoki K., Kizuki K., Moriya H., Sweeley C.C., Kamo M., Tsugita A.; "Generation of a different type of beta-kallikrein from porcine pancreatic alpha-kallikrein by the action of chymotrypsin -observation of proteolytic processing occurring around 'kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PANCREATIC TRYPOSITION.

MEDLINE-83189108; PubMed-6188842;

MEDLINE-83189108; PubMed-6188842;

MEDLINE-83189108; PubMed-6188842;

Refined 2.5 A X-ray crystal structure of the complex formed by porchine kallikrein A and the bovine pancreatic trypsin inhibitor.

Crystallization, Patterson search, structure determination, crystallization, Patterson search, structure determination, bovine trypsin-pancreatic trypsin inhibitor components and with J. Mol. Biol. 164:283-311(1983).
                                                                                                                                                                                                           Ischesche H., Mair G., Godec G., Fiedler F., Ehret W., Hirschauer Lemon M., Fritz H., Schmidt-Kaerner G., Kutzbach C.; "The primary structure of porcine glandular kallikreins."; Adv. Exp. Med. Biol. 120:245-260(1979).
                                                                                                                                                                                                                                                                                                                                                                       "The primary structure of the kallikrein from porcine pancreas."; Thesis (1976), University of Munich, Germany.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-GAY CRYSTALLOGRAPHY (2 ANGSTROMS), AND REVISIONS.
MEDLINE-83189107; PubMed=6551452;
Bode W., Chen Z., Bartels K., Kutzbach C., Schmidt-Kastner G.,
                   SEQUENCE OF 1-15 AND 95-102.
MEDLINE-89230643; PubMed=3246048;
Kamada M., Aoki K., Ikekita M., Kizuki K., Moriya H., Kamo M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-82194877; PubMed=7043199;
Fiedler F., Fink E., Tschesche H., Fritz H.;
"Porcine glandular kallikreins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autolysis loop, region.";
Chem. Pharm. Bull. 38:1053-1057(1990).
                                                                                                                                                                                                                                                                                                                    OF 8-87; 95-127 AND 176-246.
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                                                                                                                                                                             SEQUENCE OF 8-87 AND 95-246.
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                                                                                                                                                       MEDLINE=89062455; PubMed=3159.708;
I Tomiya N., Yamaguchi T., Awaya J., Kurono M., Endo S., Arata Y.,
I Takhashi N., Ishihara H., Mori M., Tejima S.;
I Takhashi N., Ishihara H., Mori M., Tejima S.;
I Takhashi N., Ishihara H., Mori M., Tejima S.;
I Takhashi N., Ishihara H., Mori M., Tejima S.;
Biochemistry 27:1146-7154(1988).
I Proceed to a superagine-linked oligosaccharides of porcine pancreatic Allikreins.
I Kininogen to release Lys-bradykinin.
I CATALYTIC ACTIVITY: Preferential cleaves Met-Lys and Arg-Ser bonds in kininogen to release Lys-bradykinin.
I CATALYTIC ACTIVITY: Preferential cleaves of Arg-|-Xaa bonds in small in olecule substrates. Highly selective action to release kallidin (lysyl-bradykinin) from kininogen involves hydrolysis of Met-|-Xaa or Leu-|-Xaa.
I SUBUNIT: Monomer.
I SUBUNIT: Monomer.
I SUBUNIT: Belongs to peptidase family Sl. Kallikrein subfamily.
I CAUTION: Native porcine kallikrein is a monomer. Chains of the parcealic beta kallikrein are heterogeneous artifacts of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Serine protease; Glycoprotein; Pancreas; 3D-structure;
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                                        Mittl P.R.E., di Marco S., Fendrich G., Pohlig G., Heim J., Sommerhoff C., Fritz H., Priestle J.P., Gruetter M.G., Structure 5:585-585(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLANDULAR KALLIKRBIN.
KALLIKRBIN (AUTOLYSIS) LOOP.
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InterPro; IRR001354; Peptidase_S1.
InterPro; IRR001314; Peptidase_S1A.
Pfam. PF001099; LYDASIN, 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00220; Tryp_SF0; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                          STRUCTURE OF CARBOHYDRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDB; 2PKA; 19-JUL-84.
PDB; 2KAI; 15-OCT-91.
PDB; 1HIA; 24-DEC-97.
MEROPS; S01.160; -.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIM=CZech II; TISSUE=Manmary gland;

KIALINE=2238257; PubMed=12477932;

KIALINE=2238257; PubMed=12477932;

KIALINE=2238257; PubMed=12477932;

KIALINE S.D., Collins F.S., Wagner L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schenen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley N.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S., Mala N., Mull M., Madan A., Rodrigues S., Sanchez A.,

Rahey J., Helton B., Young A.C., Shevchenko Y., Boutfard G.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome
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SIRAIN=BALB/c; TISSUE=Hippocampus;
MEDLINE=953.48817; PubMed=7623137;
Chen Z.-i. Yoshina S., Kato K., Momota Y., Suzuki J., Tanaka T.,
Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.;
"Expression and activity-dependent changes of a novel limbic-serine protease gene in the hippocampus.";
J. Neurosci. 15:5088-5097(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 1; Length 246;
Pred. No. 4.3;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        784 "; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                          27170 MW; 5991CEDE406A19A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  061953,
15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UR-2004 (Rel. 43, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8)
KLK8 OR PRSS19 OR NRPN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 AA
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ilarity 77.8%;
Conservative
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  36 VLVNPKWVL 44
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Best Local Similarity
7, Conserve
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246 AA;
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SEQUENCE FROM N.A.
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SEOURNCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
ENZYME REGULATION: Strongly inhibited by dIIsopropyl
fluorophosphate, leupeptin and (4-amidinophenyl)methanesulfonyl 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF N-TERMINUS, AND CHARACTERIZATION.
STRAIN=BALB/C; TISSUB=Brain;
MEDLINE=9825202; PubMed=9556608;
Shidizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K.,
Shiosaka T., Midorikawa K., Kamachi T., Kawabe A., Shiosaka S.;
"Characterization of recombinant and brain neuropsin, a
plasticity-related serine protease.";
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SIMILARITY).
  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Genzation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences "; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Gaps
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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2013 (Rel. 41, Last annotation update)
protease 1).
KLK8 OR PRSS19 OR NRPN OR BSP1.
                           N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                              28523 MW; BESF6F6BE37CD60E CRC64;
                                                                                                                                                                                                                                                                                         Query Match 80.9%; Score 38; DB 1; Best Local Similarity 77.8%; Pred. No. 4.5; Matches 7; Conservative 1; Mismatches
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61 VLVGDRWYL 69
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1 VLVNERWVL
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SEQUENCE FROM N.A.
TISSUE-Venom gland;
MEDLINE=95110313; PubMed=7811255;
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Similarity 66.7%;
6; Conservative 2
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HSSP; P00761; 1EPT.
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Best Local Similarity
Matches 6; Conserv
FROM N.A.
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RYP PLEPL
D TRYP PLEPL
C P35034;
T 01-FEB-1994 (Rel. 28, Last sequence update)
T 01-FEB-1994 (Rel. 41, Last annotation update)
T Typsin precursor (BC 3.4.21.4).
S Pharonectes platessa (Plates)
C Actinopterygii; Neopterygii; Teleostei; Neteleostei;
C Actinopterygii; Neopterygii; Teleostei; Duteleostei; Necteleostei;
C Acanthomorpha; Acanthopterygii; Percomorpha; Peuronectidae;
C Pleuronectoidei; Pleuronectidae; Pleuronectes.
N NCBI TaxID=8262;
                        MEDLINE=98389725; PubMed=922524;
Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;
Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;
Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;
J. Storine proteases in rodent hippocampus.";
J. EUNCTION: Suggested to be involved in kindling epileptogenesis and hippocampal plasticity. Has a strong proteolytic activity against fibronectin (By similarity).
J. CARALYTIC ACTIVITY: Preferential cleavage: Arg., Lys.
J. SUBCELLUIAR LOCATION: Secreted (By similarity).
J. SUBCELLUIAR LOCATION: Secreted (By similarity).
J. SUBCIPICITY: Restricted to hippocampus.
J. SIMILARITY: Belongs to peptidase family SI. Kallikrein subfamily.
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InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001234; Peptidase_S1.
InterPro; IPR001234; Peptidase_S1.
InterPro; IPR001234; Peptidase_S1.
Pfam; PF00089; trypsin; 1.
PR0072; CHYMOTRYSIN.
SMART; SR00020; TRYPSIN.
PROSTIE; PS50240; TRYPSIN DOM; 1.
PROSTIE; PS00134; TRYPSIN LHS; 1.
PROSTIE; PS00134; TRYPSIN LHS; 1.
PROSTIE; PS00134; TRYPSIN SER; 1.
Hydrolase; Serine protease; Glycoprotein; Signal.
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HSSP; Q61955; 1NPM.
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         TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIFICITY (BY SIMILARITY)
TISSUE-Liver;
Leaver M.J., George S.G.;
Submitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: Belongs to peptidase family S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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VSP4_TRIMU

TIMU

COPICATION

CONTROL (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DC Trimeresurus mucrosquamatus (Taiwan habu).

OC Trimeresurus forcas, Chordata, Craniata, Vertebrata; Euteleostomi;

OC Lepidosauria; Squamatus; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Crotalinae; Protobothrops.
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Pred. No. 6.7;
2; Mismatches 1; Indels
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REQUIRED FOR SPECIFIC:
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"Characterization of one novel venom protease with beta-fibrinogenase activity from the Taiwan habu (Trimereseurus mucrosquamatus): purification and CDNA sequence analysis.";

Biochem. Biophys. Res. Commun. 205:1707-1715(1994).

-! FUNCTION: Thrombin-like snake venom serine protease. Cleaves beta-chain of fibrinogen molecules efficiently and shows relatively lower activity on alpha-chain, with almost no activity on gamma-

    -!- SUBCELLULAR LOCATION: Secreted.
    -!- TISSUE SPECIFICITY: Expressed by the venom gland.
    -!- SIMILARITY: Belongs to peptidase family S1. Snake venom subfamily.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | MEROPE'S SULLIBS; -...
| R MEROPS; SULLIBS; -...
| R InterPro; IPR001254; Peptidase_S1.
| InterPro; IPR001254; Peptidase_S1.
| InterPro; IPR001214; Peptidase_S1.
| R InterPro; IPR001214; Peptidase_S1.
| R RONSTER; SEGOCGO; TRYPESIN DEM; 1.
| R RONSTER; PSGOCGO; TRYPESIN DEM; 1.
| R ROSTIE; PSGOLGO; TRYPESIN DEM; 1.
| R ROSTIE; PSGOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X83225; CAA58225.1; -- HSSP; P00763; 1DPO.
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                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
         activity from the Taiwan habu (Trimeresurus mucrosquamatus):
purification and cDNA sequence analysis.";
Biochem. Biochys. Res. Commun. 205:1707-1715(1994)
-!- FUNCTION: Thrombin-like snake venom serine protease. Cleaves betachain of fibrinogen molecules efficiently and shows relatively lower activity on alpha-chain, with almost no activity on gamma-
                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: Expressed by the venom gland. SIMILARITY: Belongs to peptidase family S1. Snake venom subfamily.
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MUCROFIBRASE 4
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SHARD SIMILARITY.
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InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1A.
Pfan; PF00089; trypsin; 1.
PRINTS; PR00122; CHYMOTRYPSIN.
SMARY; SM00200; TryPSSP; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
Hydrolase; Serine protease; Zymogen; Signal.
                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted TISSUE SPECIFICITY: Expressed 1
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Best Local Similarity 75.0
Matches 6; Conservative
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STANDARD; Viperidae, Crotalir NCBI\_TaxID=103944; SEQUENCE FROM N.A. TRIMU NECT TRIME ID VSP7 TRIME OPDG84; RESULT 

16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
Mucrofibrase 5 precursor (EC 3.4.21.-).
Trimeresurus mucrosquamatus (Taiwan habu).
Itimeresurus Squamata; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae, Crotalinae; Protobothrops.

TISSUE=Venom gland; MEDLINE=95110313; PubMed=7811255; Hung C.-C., Huang K.F., Chiou S.-H.;

SEQUENCE FROM N.A.

TISSUE=Venom gland

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16-007-2001 (Rel. 40, Last sequence update)
16-007-2003 (Rel. 41, Last sequence update)
SerFBB-2003 (Rel. 41, Last annotation update)
Serpentokallikrein-2 precursor (EC 3.4.21.-).
Trimeresurus mucrosquamatus (Taiwan habu).
Trimeresurus chordata; Craniata; Vertebrata; Buteleostomi; Lepidosauria; Squamata; Scleroqlossa; Serpentes; Colubroidea;
                  . .) (POTENTIAL)
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                                                                      Score 37; DB 1; Length 257;
Pred. No. 6.9;
                                                                                                                    1; Indels
                                       FCCF64A8EAF2827D CRC64;
                                                                                                                    1; Mismatches
                                         28164 MW;
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75.08;
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Best Local Similarity
Matches 6; Conserv
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TRIMU

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"Accelerated evolution of crotalinae snake venom gland serine
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Matches
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                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                       HASE, PRO7631 LDPO.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001254; Peptidase_S1.

R PRINTS; PR00122; CHYMOTRYPSIN.

R PROSITE; PS00134; TRYPSIN DGM; 1.

R PROSITE; PS00135; TRYPSIN DGM; 1.

R PROSITE; PS00135; TRYPSIN DGM; 1.

R PROSITE; PS00135; TRYPSIN LIS; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

T PROPEP 19 24 BY SIMILARITY.

T CHAIN 25 257 CHARGE RELAY SYSTEM (BY SIMILARITY).

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       Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes; Colubroidea;
Nyiperidae, Crotalinae, Trimeresurus.
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TISSUBE-Venom gland;
MEDLINE=97096898; PubMed=8941719;
MEDLINE=97096898; PubMed=8941719;
Deshimaru M., Ogawa T., Nakashina K., Nobuhisa I., Chijiwa T.,
Shimchigashi Y., Fukumaki Y., Niwa M., Yamashina I., Hattori S.,
Ohno M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .) (POTENTIAL)
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Pred. No. 6.9;
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1/2 C 013062;

1/2 C 013062;

1/3 C 013062;

1/3 C 013062;

1/4 C 013062
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75.0%;
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Best Local Similarity 75...
6, Conservative
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257 AA;
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Gaps
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=7165;
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N-LINKED (GLCNAC. . . ) (POTENTIAL).
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CHARGE RELAY SYSTEM (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR InterPro; JOLILBS; -: Cys_Ser_trypsin.

DR InterPro; IPR001254; Peptidase_S1.

DR InterPro; IPR001314; Peptidase_S1A.

DR RIMIS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR SMART; SM0020; Tryp_SRC; 1.

PROSITE; PS00134; TRYPSIN_DM; 1.

PROSITE; PS00135; TRYPSIN_HIS; 1.

R PROSITE; PS00135; TRYPSIN_HIS; 1.

TRYPSIN BRS; 1.

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Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTR2_ANOGA STANDARD; PRT; 258 AA. 017025; 017026; C. Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) CHYM2.
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STRAIN=Suakoko; TISSUE=Midgut;
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75.0%;
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HSSP; P00763; 1DPO.
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257 AA;
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Query Match
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CHYMCTRYPSIN 2.
CHAGE RELAY SYSTEM (BY SIMILARITY).
CHAGE RELAY SYSTEM (BY SIMILARITY).
CHAGE RELAY SYSTEM (BY SIMILARITY).
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BY SIMILARITY.
REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SEQUENCE FROW N.A.
STRAIN-Suakoko, TISSUE-Midgut;
STRAIN-Suakoko, TISSUE-Midgut;
Mueller H.M., Carteruccia F., Crisanti A.;
Mueller gambiae locus containing the sequences of two closely
related chymotrypsin-like proteases induced in the gut following blood
meal.";
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
-: CATALLYIT CATIVITY: Preferential cleavage: Tyr-|-Xaa,
-: TISSUE SPECIFICITY: Midgut.
-: TISSUE SPECIFICITY: Midgut.
-: DEVELOPMENTAL STAGE: Induced in the midgut of female after blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Q27289;
01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
Chymotrypsin 1 precursor (EC 3.4.21.1).
CHYMILS
Anopheles gambiae (African malaria mosquito).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1A.
Proposes; Lrypsin, 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_BER; 1.
PROSITE; PS00135; TRYPSIN_BER; 1.
Hydrolase; Serine protease; Signal; Zymogen; Digestion; Multigene family.
Interpropriate protease; Signal; Zymogen; Signal.
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LGH -> FPD (IN REF. 1).
A41AD20A630BC67B CRC64;
                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to peptidase family S1.
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Best Local Similarity
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63 LLNDRWVL 70
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258 AA;
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TR1 ANOGA
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                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=SUBAKOKO, TISSUE=Midgut;
Mueller H.M., Catteruccia F., Crisanti A.;
Man Anopheles gambiae locus containing the sequences of two closely
"An Anopheles gambiae locus containing the sequences of two closely
related chymotrypsin-like proteases induced in the gut following blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
                                                                                                                                                                                                                                                                                                  Phe-|-Xaa, Leu-|-Xaa.
-!- TISSUE SPECIFICITY: Midgut.
-!- DEVELOPMENTAL STAGE: Induced in the midgut of female after blood
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Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBL_TaxID=7165;
                                                                                                                                                                                                                                                             Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Trp-|-Xaa,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                Submitted (NOV-1992) to the EMBL/GenBank/DDBJ databases

    !- SIMILARITY: Belongs to peptidase family S1.

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                                                     SEQUENCE FROM N.A.
STRAIN=Suakoko; TISSUE=Midgut;
Mueller H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27717 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z18887; CAA9325.1; -.
EMBL; Z32645; CAA83568.1; -.
BJR; S49129; S49129.
HSSP; P00761; 1EPT.
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75.0%;
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63 LLNDRWYL 70
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333 2
119 11
212 2
59 1
206 2
259 AA;
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wes 6; Conserv
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    enzymatic activity.
    SUGCELLUIAR LOCATION: Secreted.
    TISSUE SPECIFICITY: Expressed by the venom gland.
    SIMILARITY: Belongs to peptidase family S1. Snake venom subfamily.

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R InterPro; IPR001254; Peptidase S1.

InterPro; IPR00114; Peptidase S1.

R InterPro; IPR00114; Peptidase S1.

R PRINTS; PR00121, CHYMOTRYSIN.

R SMART; SMOROOS, TryPSSIN.

R SMART; SSC040; TRYPSSIN.

PROPER

1 18 BY SIMILARITY.

T DISULFID 100 258 BY SIMILARITY.

T CARBOHYD 124 124 N'LINNED (GLCNAC. .) (POTENTIAL).

T CARBOHYD 124 124 N'LINNED (GLCNAC. .) (POTENTIAL).

T CARBOHYD 253 253 N'LINNED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Snake venom serine protease-like protein. Has lost two of the three essential catalytic residues and so probably has no
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM DATA

Lu Q.M., Jin Y., Wei J.F., Wang W.Y., Xiong Y.L.;

Lu Q.M., Jin Y., Wei J.F., Wang W.Y., Xiong Y.L.;

"CDNA cloning of serine proteinases from the venom of Trimeresurus
   28-FEB-2003 (Rel. 41, Last annotation update)
Venom serine proceinase-like protein precursor (SP1).
Trimeresurus jerdonii.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eupidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
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013057;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-B-FEB-2003 (Rel. 41, Last annotation update)
Venom serine proteinase 2 precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF292110; AAG10788.1; -.
HSSP; P00763; 1DPO.
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Similarity 75.0%;
6, Conservative
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260 AA;
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..)
                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUB-Venom gland;
MEDLINE-97056898; PubMed-8941719;
Deshinaru M., Ogawa T., Nakashima K., Nobuhisa I., Chijiwa T.,
Shimohigashi Y., Fukumaki Y., Niwa M., Yamashina I., Hattori S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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INTERPRO) IPRO01254, Peptidase_S1.
INTERPRO) IPRO01254, Peptidase_S1.
INTERPRO) IPRO01254, Peptidase_S1.
INTERPRO) IPRO01344, Peptidase_S1A.
FRINTS; PRO00369; LTYPSSIN.
SMART; SMOODO20; TTYPSSIN.
PROSITE; PSSO240; TTYPSSIN DOM; 1.
PROSITE; PSSO134; TRYPSIN_DIM; PALSE_NEG.
PROSITE; PSO0134; TRYPSIN_LIS; PALSE_NEG.
R PROSITE; PSO0135; TRYPSIN_SIN; PALSE_NEG.
R PROSITE; PSO0135; TRYPSIN_SIN; PALSE_NEG.
R PROPER 1 18 BY SIMILARITY.
I PROPEP 24 BY SIMILARITY.
I PROPEP 25 BY SIMILARITY.
I PROPEP 25 BY SIMILARITY.
I PROPEP 26 BY SIMILARITY.
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Trimeresurus.
NCBI_TaxID=88087;
                                                                                                                                                                                                                                                                                                                                                                                                                                        "Accelerated evolution of crotalinae snake venom gland serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          유
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Pred. No. 7;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Probable arginyl-tRNA--protein transferase (EC 2.3.2.8)
transferase) (Arginyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DODOA5394CBF9B4A CRC64;
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55.6%;
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55 ILINQEWUL 63
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260 AA;
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Best Local Similarity
Matches 5; Conserv
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ATE PSEPK
ID ATE PSEPI
AC Q88FS6;
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TLF2. Trimeresurus flavoviridis (Habu). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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19q13.3-q13.4.
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ACT_SITE
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                                                                                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDINE-22423060; PubMed=12534463;

Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,

Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,

A Brinkec L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,

A Madupu R., Nelson M., White O., Peterson J., Khouri H., Hance I.,

Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazez A.,

A Utterback T., Rizzo M., Lee K., Kosack D., Mosetl D., Wedler H.,

A Lauber J., Strippandic D., Hoheisel J., Straetz M., Heim S.,

A Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tummmler B.,

Riswitz C.M.; Timme sequence and comparative analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser C.M.;
"Comparative analysis of the
"Comparative analysis of the
metabolically versatile Pseudomons putida KT2440.";
metabolically versatile Pseudomons putida KT2440.";
Environ. Microbiol. 4:799-808(2002).
-!- FUNCTION: Functions in the N-end rule pathway of protein
degradation where it conjugates Arg from its aminoacyl-tRNA to th
N-termini of proteins containing an N-terminal aspartate or
glutamate (Potential).
-!- CATALXTIC ACTIVITY: L-arginyl-tRNA + protein = tRNA + L-arginyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UXEO, Q9UKR1,
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Kallikrein 12 precursor (BC 3.4.21.-) (Kallikrein-like protein (KLK-LS).
                        Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e; Acyltransferase; Complete proteome.
235 AA; 27889 MW; F9C30B85BCDAE860 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic (Potential). SIMILARITY: Belongs to the R-transferase family.
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MEDLINE=20118156; PubMed=10652563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE016788; AAN69600.1; -.
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225 LLINQRWV 232
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                                                                                                                NCBI_TaxID=160488,
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PP4006
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LKC_HUMAN
D__KLKC_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isoId=Q9URR0-2; Sequence=VSP_005403;
-!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).

Yousef G.M., Magklara A., Scorilas A., Diamandis B.P.;

Cloning of new alternatively spliced forms of the kallikrein-like gene 5 (KLK-L5).";
Yousef G.M., Luo L.-Y., Diamandis B.P.; "Identification of novel human kallikrein-like genes on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
MEDILINE=20510090; PubMed=11054574;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.
Moss P., Paeper B., Wang K.;
"Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region.";
Gene 257:119-130(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS, SOL. 1020; --.
Genew; HGNC: 6360; KLK12.
MIN, 605239; --.
GO; GO: 0004252; F: Serine-type endopeptidase activity; NAS.
GO; GO: 0006508; P: Proteolypais and peptidolysis; NAS.
InterPro; IPR001003; Cys. Ser. trypsin.
InterPro; IPR001254; Peptidase_31.
InterPro; IPR001314; Peptidase_31A.
                                                                                                                                                                                                                            gene 5 (KLX-L5).";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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(BY
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PRINTS; PR00122; CHYMOTRYPSIN.

SMART; SM00120; TRYPSIN 1.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

HYDGOLSSE; SS00135; TRYPSIN SER; 1.

Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KALLIKREIN 12.
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=09UKR0-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                            19q13.3-q13.4.";
Anticancer Res. 19:2843-2852(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF135025; AAD26426.2; ... EMBL; AF135025; AAF06055.1; -. EMBL; AF243527; AAG33365.1; -. EMBL; AC011473; AAG23258.1; -. HSSP; P00763; 1DPO.
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SEQUENCE
 ACT SITE
DISULPID
DISULPID
DISULPID
DISULPID
DISULPID
CARBOHYD
CARBOHYD
VARSPLIC
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1 VLVNERWVL 9 ||::|||| 50 VLIDHRWVL 58

.; 0

0; Gaps

Query Match

76.6%; Score 36; DB 1; Length 248;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 1; Indels

sarch completed: March 1, 2004, 17:29:57
bb time : 7 secs

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screening for stratum corneum cnymotrypsin enzyme (SCCE). Froceases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is
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30	Human s	stratum		corneum		HOE.	chymotrypsin enzyme	peptide #5	(residues	6-14).
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2	cancer;		ian	Ä	18t;	lun	g; colon;	state; carcin	hum	
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PF	07-FEB-2001		, 20	2001WO-US003977	15003	977				
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X E E	Diagnosing		cancer		compris	868	detecting s	stratum corneum	chymotrypsin	sin
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S &	Claim 2	 ເດ	Page	103;	127pp;		English.			
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Length 9;

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ADA05736 standard; protein; 198 AA.
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05-OCT-2001, 2001US-0327435P.
05-OCT-2001, 2001US-0327917P.
09-OCT-2001, 2001US-0328029P.
09-OCT-2001, 2001US-0328049P.
09-OCT-2001, 2001US-0328849P.
15-OCT-2001, 2001US-0328849P.
15-OCT-2001, 2001US-0328849P.
17-OCT-2001, 2001US-0330142P.
18-OCT-2001, 2001US-0330162P.
22-OCT-2001, 2001US-0341058P.
24-OCT-2001, 2001US-0341058P.
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N-PSDB; ADA05735.
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16-MAY-2002; 2
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1-NOV-2001;
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22-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polymuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (POR) primers, ollgomers, and for chomosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal extivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic gene mapping, identification of mutations responsible for genetic gene mapping, identification of mutations responsible for genetic sequences and conducts dependent on DNA and amino acid sequences. Abg000010-Abg30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at the printed specification, but was obtained in electronic format directly from MIPO at
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                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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                                      Indels
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                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #23369.
                                                                                                                                                                                                         ABG23378 standard, protein, 136 AA.
100.001
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23-AUG-2000; 2000US-00649167
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                 immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
numan; NOVX; antidiabetic; anorectic; antibacterial; virucide;
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WO2003029424-A2

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more described above and a carrier; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for determining the presence or acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for cabove; (10) a method for identifying a potential therapeutic agent for a pathology associated with the polypeptide; (11) a method of a pathology associated with the above polypeptide; (11) a method of a pathology associated with the above polypeptide; (11) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a method for producing the above polypeptide in a method for producing the above polypeptide or the nucleic and molecule may be used to diagnose, treat or prevent metabolic asyndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic cat metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, probes, in chromosome mapping, tissue typing, prevents and probes; in chromosome mapping, tissue typing, prevents a polyperied on the prese New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or Claim 1; Page 170; 586pp; English.

Sequence 198 AA;

Gaps ö 100.0%; Score 40; DB 6; Length 198; 100.0%; Pred. No. 14; tive 0; Mismatches 0; Indels Local Similarity 100. Query Match Best Loc Matches

Q 1 LIPIOILLI ADA05732 standard; protein; 250 AA

(first entry) 06-NOV-2003

Human NOV18a protein SEQ ID NO:92.

human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alaheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.

sapiens Ношо

09-0CT-2001; 2001US-0328029P. 09-0CT-2001; 2001US-0328044P. 09-0CT-2001; 2001US-0328056F. 15-0CT-2001; 2001US-032849P. 15-0CT-2001; 2001US-0332844P. 2002US-0373250P. 2002US-0373815P. 2002US-0373815P. 2002US-0373845P. 2002US-037484F. 2002US-0381037P. 2002US-0381037P. 2002US-0381042P. 2002US-0381642P. 2002US-0381642P. 2002US-0381642P. 2001US-0330309P. 2001US-0341058P. 2001US-0339266P. 2001US-0343629P. 2001US-0346357P. 02-OCT-2002; 2002WO-US031373 19-APR-2002; 19-APR-2002; 22-APR-2002; 19-APR-2002;

(CURA-) CURAGEN CORP.

Dipippo VA; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Bhinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dibippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36

N-PSDB; ADA05731.

.. 0

obesity, or New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing pharmacogenomics

Claim 1; Page 169-170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOVI). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a cell
comprising the nucleic acid molecule described above; (5) a cell
prise to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
coplypeptide or nucleic acid molecule in a first mammalian subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
the intracting a pathology that is related to an aberrant expression or
aberrant physiological interactions of the polypeptide; (11) a method of
screening for a modulator of activity or of latency or predisposition to

Sequence 253 AA;

field.)

SXS

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a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide. Norw sequences have antidabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, anorectic, antibacterial, virucide, and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a polypeptide is useful in manufacturing a medicament for treating a soid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders used as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various distingation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. B. coli) or eukaryotic and testing of cpds. useful for treating or preventing conditions associated with beta-amyloid peptide, esp. Alzeimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human amyloid precursor protein protease - used to develop prods. for the treatment or diagnosis of associated conditions, esp.
                          Gaps
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100.0%; Score 40; DB 2; 100.0%; Pred. No. 18;
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                         0; Mismatches
                                                                                                                                                                                                                           Human amyloid precursor protein protease.
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ABB84421
ID ABB84421 standard; peptide; 253 AA.
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                                                                                                                                              AAW05383 standard; protein; 253 AA
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 Query Match
Best Local Similarity 100.
Matches 9; Conservative
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N-PSDB; AAT39783.
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Best Local S
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Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of specific inhibitors

Egelrud I, Hansson L;

(SYMB-) SYMBICOM AB.

WPI; 1995-052088/07.

N-PSDB; AAQ81203.

Disclosure, Page 97; 137pp; English.

The enzyme encoded by this sequence is used in pharmaceutical, cosmetic and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkeratotic conditions (e.g. callosities or keratosis pilaris), ichthyoses, psoriasis, eczema, etc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid p5507. (Updated on 25-MAR-2003 to correct PN

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ABB84421;
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08-NOV-2002 (first entry)

Human SCCE protein N-terminal fragment SEQ ID 48.

SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.

Homo sapiens.

WO200262135-A2.

15-AUG-2002,

08-FEB-2002; 2002WO-IB001300.

09-FEB-2001; 2001CA-02332655. 09-FEB-2001; 2001DK-0000218.

(EGEL/) EGELRUD T. (HANS/) HANSSON L.

Egelrud T, Hansson L;

WPI; 2002-643380/69

Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.

Example 6; Page 37; 74pp; English.

This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence coding at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous scce or its variant in skin. The product of the invention is useful as a model to the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or resting of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an inflammatoxy skin diseases selected from diseases consisting of epidermal inflammation, pruritus, acopic dermatitis, eccame, acne and inherited skin diseases with epidermal hyperkeratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases where itch is a composition for relieve of various skin diseases where itch is a composition for presents the N-reminal fragment of the human stratum corneum chymotryptic enzyme, SCCE synonymous with human kallikrein 7 (KLK7), used in the development of the transgenic mammals described in the invention where itch is a component. fragment of the human strat

Gaps ö 100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 18; cive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 9; Conservative

1 LLPLQILLL 9

Sequence 253 AA;

ABB84406 standard; protein; 253 AA.

ABB84406;

(first entry) 08-NOV-2002

Human SCCE protein.

SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; prunitus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.

Homo sapiens

WO200262135-A2.

15-AUG-2002.

38-FEB-2002; 2002WO-IB001300.

09-FEB-2001; 2001CA-02332655. 09-FEB-2001; 2001DK-00000218.

(EGEL/) EGELRUD T. (HANS/) HANSSON L.

ï Egelrud T, Hansson

WPI; 2002-643380/69. N-PSDB; ABQ76226.

Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.

Claim 10; Page 58-59; 74pp; English.

This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous scce or its variant in skin. The product of the invention is useful as a model or its variant in skin. The product of the invention is useful as a model or ameliorate a pathogenic condition, for development or testing of a cosmetic or apharmaceutical formulation, and for the development of a diagnostic method. It can also be useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of inflammatory skin diseases selected from diseases consisting of epidermal composition effective for the prevention or treatment of not hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation, pruritus, atopic dermatitis, eczema, acne and inherited skin diseases with epidermal hyperkeratosis. The mammal of the invention is also useful or as a model for further studies of itch mechanisms and the testing of epiderment or as a model for further studies for the menamal of the invention is also useful potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the human stratum corneum chymotryptic enzyme, SCCE which is a serine protease synonymous protease synonymous corneum chymotryptic enzyme, SCCE which is a serine protease s with human kallikrein 7 (KLK7) and is used in the development transgenic mammals described in the invention

Sequence 253 AA;

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0; Gaps 100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 18; ive 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 9; Conservative

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ESULT 8 BB84406

AAU82740;

(first entry) 23-APR-2002

AAU82740 standard; protein; 253 AA

Amino acid sequence of novel human protease #39.

Human, protease, cancer, immune-related disorder, cardiovascular disease, neuronal-associated disease, metabolic disorder; inflammatory disorder; neurous system disorder, sexual dysfunction, pain, mood disorder; hypertension, psychotic disorder, neurological disorder, dyskinesia, viral infection, human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme

Homo sapiens.

WO200200860-A2.

03-JAN-2002

26-JUN-2001; 2001WO-US020171

26-JUN-2000; 2000US-0214047P

(SUGE-) SUGEN INC.

Sudarsanam S, Manning G, Caenepeel S; Whyte D, Plowman G, Wi Charydczak G;

Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory WPI; 2002-139913/18. N-PSDB; ABK31782

Claim 6; Fig 2N; 313pp; English.

disorders.

The present invention relates to the isolation of novel human proteases, and the mucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. inflammatory diseases, metabolic coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obssity), inflammatory disorders (e.g. diabetes, obssity), inflammatory disorders (e.g. disorders, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's cisease) and dyskinesias. The nucleic acids and polypeptides are also virus (HIV), and non-viral infections caused by human immunodeficiency virus (HIV), and non-viral infections acused by human immunodeficiency glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel human proteases of the invention

Sequence 253 AA;

Gaps .; 0 100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 18; 0; Indels 0; Mismatches Conservative Query Match Best Local Similarity '-hes 9; Conserve

LLPLOILLL 14 1 LLPLQILLL 9

ESULT 10 BU07440

ABU07440 standard; protein; 253 AA.

ABU07440; 

(first entry) 28-JAN-2003 Protein differentially regulated in prostate cancer #43.

Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring.

Homo sapiens.

WO200281638-A2.

17-0CT-2002.

08-AFR-2002; 2002WO-US010824

06-AFR-2001; 2001US-0281731P.

(ORIG-) ORIGENE TECHNOLOGIES INC.

Jay G; Sun Z,

WPI; 2003-058520/05 N-PSDB; ABX10343 Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

Claim 1; Page 293-294; 416pp; English.

The invention describes genes (I) which are differentially regulated in prostate cancer. (I) is useful for diagnosing a prostate cancer in a sample comprising profested tissue, which involves determining the number of the probability that the sample comprises the number is indicative of the probability that the sample comprises the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises of target genes which are differentially-regulated in prostate cancer. (I) is useful for identifying a prostate cancer, which involves concerned a spoke useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated cancer cells, which involves contacting a polypeptide differentially-regulated concerned in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) the test agent to modulate a biological activity of the polypeptide, and concerned in prostate cancer cells with a test agent under conditions especially relating to prostate cancer. (I) and its expression of products are used in the diagnostic test to assay for presence of cancer. (I) is useful and diagnostic test to assay for presence of cancer of cancer, its stage of development, the nature of genetic defect, etc. (I) and issue sections, in biopsy sample, in total NM, in lymph, in bloopsy and concerned in propagate and the delinest cancer. (I) and stage of development, the nature of genetic defect, etc. (I) and specific binding partners of the polypeptide and thus concerned in therapeutic applications to treat prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways and the delinest of a protein differentially the are useful in disagnostic, ther regulated in prostate cancer

Ą. Sequence 253

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Gaps

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Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
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molecular marker; drug target; cancer detection; cancer diagnosis;
cancer staging; cancer grading; cancer assessing; cancer monitoring.
                6; Length 253;
                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Protein differentially regulated in prostate cancer #74.
                    DB
                                                              Mismatches
                Score 40;
Pred. No. 1
                                                                                                                                                                                                                                                             ABU07471 standard; protein; 253 AA.
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                  100.0%;
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                                                                                                                                                                                                                                                                                                                                              (first entry)
Query Match
Best Local Similarity 100.
                                                                                                                                                LLPLOILLL 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jay G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises for prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue in target genes which are differentially-regulated in prostate cancer. Preferably, the expression levels in a sample comprising prostate cancer. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is uncein a smolecular markers, as drug targets, and for detecting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosing, stading, grading, assessing, monitoring, prognosticating, preventing or treating, determining predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in blood etc. (I) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. The polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus
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Matches

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Query Match Best Local Similarity

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RESULT 13

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for searching specific binding partners of the polypeptide. (1) is useful in therapeutic applications to treat prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways physiologically relevant to prostate cancer permits the definition of functional and disease pathways and the delineation of targets in these pathway which are useful in diagnostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein differentially regulated in prostate cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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100.0%; Pred. No. 18;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR58471 standard; protein; 253 AA.
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30-MAY-2002; 2002US-0384531P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
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Human HSCEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method of detecting an ovarian cancer-
associated transcript in a cell from a patient, by contacting a
biological sample from the patient with a polynucleotide that selectively
hybridizes to a sequence at least 80% identical to any of one of 80
nucleic acid sequences given in the specification. The method is useful
in diagnosing ovarian cancer and in identifying and using agents and/or
targets that inhibit ovarian cancer. The nucleic acid molecule,
polypeptide and the antibody may also be used in detecting ovarian
cancers, monitoring and early detection of relapse following treatment,
monitoring response to therapy, selecting patients for post-operative
chemotherapy or radiation therapy, in selecting mode of therapy,
and as vaccines. This sequence corresponds to one of the proteins used
for the detection method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
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                                                                                                                                     cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection.
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                                                                                                             Ovarian cancer-associated protein #24
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                 ADB80484 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Page 291; 332pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                  (EOSB-) EOS BIOTECHNOLOGY INC
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05-SEP-2001; 2001US-0317544P
13-NOV-2001; 2001US-0350666P.
12-APR-2002; 2002US-0372246P.
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N-PSDB; ADB80483.
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tes 9; Conserv
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                                               ADB80484;
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Matches
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 DB80484
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The present sequence is human stratum corneum chymotryptic enzyne (HSCEB), a member of the kallikrein multi-gene family. Kallikreins and kallikrein-like proteins are a subgroup of the serine proteins enzyme family. They catalyse the selective cleavage of specific polypeptide precursors to release peptides with potent biological activity. Nucleic cids encoding kallikrein-like proteins KKK-Li, KKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gastric cancer associated antigen protein sequence SEQ ID NO:942.
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Human, Kik-Li; Kik-Li; Kik-Li; Kik-Li; Kik-Li; Kik-Li; Kik-Li; HSCEE;
human stratum corneum chymotryptic enzyme; kallikrein-like protein;
serine protease; cytostatic; cancer; prostrate cancer.
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99US-0127386P.
99US-0144919P.
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21-JUL-1999;
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AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 propresent nucleotide sequences encoding human breast, gatartic and prostate cancer associated antigen precursors (CAAP) respectively.

AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gatartic and prostate (CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein, e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 625; 799pp; English.
                                                                                                                          (LUDW-) LUDWIG INST CANCER RES
99US-0136526P.
99US-0153454P.
                                                                                                                                                                                                                                                                                         WPI; 2001-025274/03.
28-MAY-1999;
10-SEP-1999;
                                                                                                                                                                                                                Obata Y;
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Sequence 142 AA;

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earch completed: March 1, 2004, 17:28:52 ob time: 46.5556 secs

Ouery Match

95.0%; Score 38; DB 4; Length 142;
Best Local Similarity 88.9%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 0; Indels

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0; Gaps

1 LLPLOILLL 9 |||||:||| 48 LLPLOLLLL 56

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Sequence 2, Appli
Sequence 3, Appli
Sequence 2, Appli
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Sequence 3, Appli
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Sequence 12075, Appl
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Sequence 6, Appli
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    (without alignments)
    39.081 Million cell updates/sec
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Sequence 2,
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Sequence 3
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Sequence 3
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-918-243-35
US-08-918-243-35
US-08-918-243-35
US-08-918-243-35
US-08-918-24-34-2
US-09-918-24-3
US-09-764-762-3
US-09-764-762-3
US-09-918-243-33
US-08-09-918-243-33
US-08-09-918-243-33
US-08-09-918-243-33
US-08-09-918-243-33
US-08-09-99-918-343-33
                                                                                                                                                                                                                                                                                                                                                                                                                    otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                       389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                inimum DB seq length: 0 aximum DB seq length: 2000000000
                                                                                                                                                                                                               US-09-905-083-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                                                                                                                              1 LIPLQILLL 9
                                                                                                                                                                                                                                              erfect score:
                                                                                                                                                                                                                                                                                                             coring table:
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                                                                                        4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atabase :
                                                                                                                                                                                                                                                                     equence:
                                                                                                                                                                                                                                                                                                                                                                            earched:
                                                                                                                                  in on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              esult
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Sequence 28, Appl Sequence 28, Appl Sequence 38, Appl Sequence 36, Appl Sequence 36, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli	the Barly Diagnosis of	in ength 9; Indels 0; Gaps 0;	of ovarian cancer
12 3 US-09-502-600-28 12 4 US-09-918-243-28 264 3 US-08-713-5567-42 269 3 US-08-713-5567-42 269 3 US-08-713-5567-36 395 4 US-09-489-039A-9507 402 2 US-08-472-548-2 402 2 US-08-472-548-2 402 3 US-08-472-548-4 412 2 US-08-73-48-4 412 2 US-08-73-8-4 412 2 US-08-73-8-4 412 2 US-08-73-8-4 412 2 US-08-73-8-4 412 2 US-08-73-8-67-8-4 412 2 US-08-73-8-67-8-4 412 2 US-08-73-5667-4 413 1 US-09-134-001-5063 492 1 US-07-794-393-4	Methods for	ne SCCE prote 10, DB 3, L 40. 3e+05; stches 0;	on US/09918243 imothy J. fartin J. lessandro fethods for the early diagnosis COIP/COP/CIP TOTB/COP/CIP TOTB/COP/CIP TOTB/COP/CIP 2001-07-30 mBER: US 01-07-13.
28 29 31 31 32 33 34 34 35 36 37 38 38 39 30 30 31 31 32 33 34 36 37 38 38 39 30 30 30 30 30 30 30 30 30 30	RESULT 1 US-09-502-600-35 Sequence 35, Application US/09502600A Patent No. 6294344 GENERAL INFORMATION: TITLE OF INVENTION: Compositions and TITLE OF INVENTION: Compositions and TITLE REPERENCE: D6223CIP-C FILE REPERENCE: D6223CIP-C CURRENT FILING DATE: 2000-02-11 CURRENT APPLICATION NUMBER: US/09/502 ( PRIOR APPLICATION NUMBER: US/09/502 ( NUMBER OF SEQ ID NOS: 136 SEQ ID NO 35 LENGTH: 9	TYPE: PRT CREANISM: Homo sapie FEATURE: COTHER INFORMATION: R US-09-502-600-35 Query Match Best Local Similarity Matches OY 1 LLPLQILLL Db 1 LLPLQILLL Db	RESULT 2 US-09-916-243-35 US-09-916-243-35 Sequence 35, Application US/09918243 Patent No. 6627403 GENERAL INFORMATION: APPLICANT: O'Brien, Timothy J. APPLICANT: Cannon, Martin J. APPLICANT: Santin, Alessandro ITLE OF INVENTION: Methods for the FILE OF INVENTION Methods for the CURRENT APPLICATION NUMBER: US PRIOR FILING DATE: 2001-07-30 PRIOR FILING DATE: 2001-07-30 PRIOR FILING DATE: 2001-07-30 PRIOR FILING DATE: 2001-07-30 NUMBER OF SEQ ID NOS: 136 SEQ ID NO 35 LENGTH: 9 ILENGTH: 9 TYPE: PRI CREANISM: Homo sapiens

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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                           S-08-557-146-2
Sequence 2. Application US/08557146
Sequence 2. Application US/08557146
Batent No. 5834290
GENERAL INFORMATION:
APPLICANT: Beglind, Torbjorn
APPLICANT: Beglind, Tennart
TITLE OF INVENTION: Ennart
TITLE OF INVENTION: Brayme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2187.
ZIP: 10036-2187.
COMPUTER: EACH FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: UNMBER: US/08/557,146
ATTORNEY/AGENT INFORMATION:
NAME: STEINEY INFORMATION:
NAME: STEINEY INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                            100.0%; Score 40; DB 4; Length 9; 100.0%; Pred. No. 3e+05; Live 0; Mismatches 0; Indels
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                      NAME/KEY: CHAIN
OTHER INFORMATION: Residues 6-14 of the SCCE protein
3-09-918-243-35
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0; Mismatches
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Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
S-08-557-146-2
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                                                                                                              Query Match
Best Local Similarity
Matches 9; Conserv
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Gaps
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| Sequence 2, Septication US/09154344
| Patent No. 5981256
| GENERAL INFORMATION:
| APPLICANT: Bgelrud, Torbjorn
| APPLICANT: Bgelrud, Tennart
| TITLE OF INVENTION: Enzyme (SCCE)
| TITLE OF INVENTION: Enzyme (SCCE)
| CORRESPONDENCES: 17
| CORRESPONDENCE ADDRESS:
| ADDRESSED: White & Case, Patent Department
| STREET: New York | STREET: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 2; Length 253;
Pred. No. 3;
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                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastes0 for Windows Version 2.0
SOFTWARE: Fastes0 for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMONICATION INFORMATION:
TELEPHONE: 415-885-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US/09/154,344
16-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
E: Incyte Pharmac 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 253 amino acids TYPE: amino acid
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Best Local Similarity 100.
                                                                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LLPLQILLL 9
                                                                       Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: 532504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE
                                                                                                                                                   USA
                                                               CITY: Pa.
STATE: C.
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-824-874-3
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us-09-905-083-35.rai

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100.0%; Score 40; DB 3; Length 253; 100.0%; Pred. No. 3;
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                                                            0; Indels
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3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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CLASSIPICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 40;
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US-09-764-762-3
US-09-764-762-3
Sequence 3, Application US/09764762
; Patent No. 6472195
; GENERAL INFORMATION:
                                                                                                                                                                                                                                              Sequence 3, Application US/09210084
Patent No. 6197511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
Query Match
Best Local Similarity 100.
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Best Local Similarity 100.

Matches 9; Conservative
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IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
                                                                                                                                                                                                                                US-09-210-084-3
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Patent No. 603337
GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Dixon, Eric P.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indiana
CONTY: Indiana
CONTY: United States of America
ZIP: 46285 Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/930,188
                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
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Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels
               APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSFICATION: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REGISTRATION NUMBER: 1103326-181
REGISTRATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 84-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPLOGY: linear
MOLECULE TYPE: protein
S-09-154-344-2
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PLORSIFICATION:
PLOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-APR-1955
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERRNEN/DOCKET NUMBER: X9239
TELECHONE: 317-277-1090
TELECHONE: 317-277-1090
TELEFAX: 317-277-1090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                1103326-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
IS-08-930-188-2
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IS-08-930-188-2
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Lal, Preeti
LITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
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1 LLPLOILL
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US-09-502-600-33
                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US96-04294-2
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GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID FRECURSOR PROTEIN PROTEASE AND TITLE OF SEQUENCES: 3
CORRESPONDENCES: 3
CORRESPONDENCES: 3
CORRESPONDENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
            COMPUTER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STREET: 3174 Porter Drive
CUNTRY: USA
ZIP: 94304
COMPUTER: EMA Compatible
COMPUTER: IBM Compatible
CURRENT APPLICATION NAMER: US/09/764,762
FILING DATE: I6-Jan-2001
CLASSIFICATION NUMBER: 09/210,084
FILING DATE: CURROWN>
ATTORNEY AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCEY DOCKET NUMBER: PF-0252 US
TELEFRENCEY COKET NUMBER: PF-0255
TELECOMMUNICATION INFORMATION:
TELEFRENCEY: A15-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Bli Lilly and Company STREET: Lilly Corporate Center CIT: Indianapolis STATE: Indiana States of America STATE: Indiana COUNTRY: United States of America ZIP: 46285. COMPUTER TRADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentln Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US96/04294 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 40; DB Best Local Similarity 100.0%; Pred. No. 3; Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 253 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LiPLOILL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LLPLOILLL 9
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CT-US96-04294-2
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PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/416,257
FILIND DATE: 04-APPLIDS:
ATTORNEY/ABATION: 08-APPLIDS:
ATTORNEY/ABATION: 08-APPLIDS:
NUMBER: 04-APPLIDS:
NUMBER: 04-APPLIDS: 08-APPLIDS:
NUMBER: 04-APPLIDS: 08-APPLIDS:
NUMBER: 04-APPLIDS: 08-APPLIDS: 08
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NAME/KEY: SITE
| LOCATION: (8)
| OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-1083
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APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Ryba, Nick
APPLICANT: Hoon, Mark
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the United States of America
APPLICANT: Bepartment of Health and Human Services
TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
FILE REFERENCE: 02307E-098000US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 85.0%; Score 34; DB 4; Length 73; Best Local Similarity 87.5%; Pred. No. 11; Matches 7; Conservative 1; Mismatches 0; Indels
                   EARLIER FILLING DATE: 1997-06-06
EARLIER FILLING DATE: 1997-07-05-06
EARLIER FILLING DATE: 1997-07-05-06
EARLIER FILLING DATE: 1997-07-06-06
EARLIER FILLING DATE: 1998-07-15
SOCITANER: PAPELICATION NUMBER: 60/094,657
ESARITER FILLING DATE: 1998-07-16
SSOCITANE: PAPELICATION NUMBER: 60/094,657
ESARITER FILLING DATE: 1998-07-16
SSOCITANER: PAPELICATION NUMBER: 60/094,657
ESARITER FILLING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
   60/048,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37, Application US/09393634 Patent No. 6558910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 ibioinii 32
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                                                                                                                                                                                                                                                                                                                                                             90.0%; Score 36; DB 4; Length 9; 100.0%; Pred. No. 3e+05; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                 NAME/KEY: CHAIN
OTHER INFORMATION: Residues 5-13 of the SCCE protein
S-09-918-243-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEREAL NO. 65.21/4

APPLICANT: Young et al.

APPLICANT: Young et al.

TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REPERNCE: PZ607P1

CURRENT PILING DATE: 1998-12-04

BARLIER APPLICATION NUMBER: BC7/US98/11422

BARLIER PILING DATE: 1998-6-04

BARLIER FILING DATE: 1998-6-04

BARLIER FILING DATE: 1997-06-06

BARLIER FILING DATE: 1997-06-06

BARLIER FILING DATE: 1997-06-06

BARLIER APPLICATION NUMBER: 60/048,881

BARLIER APPLICATION NUMBER: 60/048,881

BARLIER APPLICATION NUMBER: 60/048,896

BARLIER PILING DATE: 1997-06-06

BARLIER PILING DATE: 1997-06-06

BARLIER PILING DATE: 1997-06-06

BARLIER PILING DATE: 1997-06-06

BARLIER APPLICATION NUMBER: 60/048,896

BARLIER PILING DATE: 1997-06-06

BARLIER PILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1083, Application US/09205258
Patent No. 6525174
                                                                                                                                                                                                                                                                                                                                                             90.0
Best Local Similarity 100.
Matches 8; Conservative
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 33
LENGTH: 9
                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LLPLOILL 8
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S-09-205-258-1083
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EARLIER I
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Gaps

us-09-905-083-35.rai

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RESULT 15
US-09-252-991A-22870
; Sequence 22870, Application US/09252991A
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Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICATION

TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REPERENCE: POOD PU

CURRENT APPLICATION NUMBER: US/09/205,258

CURRENT FILING DATE: 1998-06-04

EARLIER FILING DATE: 1998-06-05

EARLIER FILING DATE: 1997-06-05

EARLIER APPLICATION NUMBER: 60/048,885

EARLIER APPLICATION NUMBER: 60/048,881

EARLIER APPLICATION NUMBER: 60/048,881

EARLIER APPLICATION NUMBER: 60/048,880

EARLIER APPLICATION NUMBER: 60/048,880

EARLIER APPLICATION NUMBER: 60/048,880

EARLIER APPLICATION NUMBER: 60/048,896

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,891

EARLIER APPLICATION NUMBER: 60/048,991

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,991

EARLIER APPLICATION NUMBER: 60/048,991

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,991

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-0
CURRENT APPLICATION NUMBER: US/09/393,634
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 37
LENGTH: 302
TYPE: PRT
ORGANISM: Homo sapiens
FRATURE:
OTHER INFORMATION: human GR02
NAME/KEY: MOD RES
LOCATION: (143)
COTHER INFORMATION: Xaa = any amino acid
S-09-393-634-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             j.09-205-258-1079
Sequence 1079, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 LMPIQILLM 50
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PEATURE:
NAME/KEY: SITE
LOCATION: (152)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PEATURE:
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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EARLIER PEDICATION NUMBER: 60/049,019
EARLIER PEDICATION NUMBER: 60/048,970
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER PILING DATE: 1997-66-06
EARLIER PILING DATE: 1997-66-06
EARLIER PEDICATION NUMBER: 60/049,373
EARLIER PEDICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-66-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-16
EARLIER FILING DATE: 199
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 iPiQLili 383
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NAME/KEY: SITE
LOCATION: (359)
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us-09-905-083-35.rai
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Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: ARENGINGS ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AVMERS: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22870

LENGTH: 569

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

1-09-252-991A-22870
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Pred. No. 95;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 85.0%;
Best Local Similarity 77.8%;
Matches 7; Conservative 1
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aarch completed: March 1, 2004, 17:38:24
ob time : 11.8889 secs

1 LLPLQILLL 9 |||| :||| 51 LLPLSVLLL 59

us-09-905-083-35.rapb

Seguence 2472, Ap

Sequence 39, Appl.
Sequence 37, Appl.
Sequence 1079, Appl.
Sequence 1079, Ap
Sequence 1079, Ap
Sequence 20447, A
Sequence 20447, A
Sequence 20, Appl.
Sequence 89, Appl.
Sequence 99, Appl.

Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence

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US-09-918-243-35

US-09-918-243-35

Sequence 35, Application US/09918243

Fatent No. US20020142317A1

GENERAL INFORMATION:

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REPERENCE: D6223CIP/C/D/CIP

CURRENT FILING DATE: 2001-07-30

FRIOR FILING DATE: 2001-07-30

FRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 35

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 40; DB 9; Length 9; Best Local Similarity 100.0%; Pred. No. 7.1e+05; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-918-243-35
                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-09-905-083-35
Sequence 35, Application US/09905083
Patent No. US20020146708A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                 March 1, 2004, 17:35:01 ; Search time 24.1111 Seconds (without alignments) 78.818 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. (cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2. (cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/BCT_NEW_PUB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/BCO8_BCMB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/BCO8_BCMB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
4. (cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-905-083-515-98
US-09-905-083-515-98
US-09-764-263-90
5 US-10-264-283-90
5 US-10-173-999-48
5 US-09-918-243-33
US-09-905-083-33
US-09-905-083-33
US-09-805-913A-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            809742 segs, 211153259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    M protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inimum DB seq length: 0 aximum DB seq length: 200000000
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40
1 LLPLQILLL 9
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                coring table:
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                                                                                                                                                                                                                                                                                                                                                   equence:
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No.
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Gaps

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Length 9;

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CITY: Palo Alto
                                           USA
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CRGANISM: Homo sapiens
US-10-264-283-90
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APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer FILE OF INVENTION: Ovarian Cancer FILE REPERBICE: D6223CIP/C/Div CURRENT PPILICATION NUMBER: US/09/905,083 CURRENT FILING DATE: 2001-07-13 PRIOR RILING DATE: 2000-02-11 NUMBER OF SEQ ID NOS: 136 SEQ ID NOS: 136 LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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100.0%; Score 40; DB 9; Length 253;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                              NAME/KEY: CHAIN
OTHER INFORMATION: Residues 6-14 of the SCCE protein
3-09-905-083-35
                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 40; DB 9; I
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TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PLOWARN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CARNEFEL, SEAN
APPLICANT: CRANCPELL, SEAN
APPLICANT: CRANCPELL, SEAN
APPLICANT: SUDARSANM, SUCHA
APPLICANT: SUDARSANM, SUCHA
APPLICANT: OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-66-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09764762
Patent No. US20020068341A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 98, Application US/0988615
Patent No. US20020064856A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 98
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
S-09-888-615-98
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Best Local Similarity luv.
9; Conservative
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ORGANISM: Homo sapiens
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3-09-888-615-98
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US-10-264-283-90
| Sequence 90, Application US/10264283
| Sequence 90, Application US/10264283
| Publication No. US20030144494A1
| GENERAL INFORMATION:
| APPLICANT: Algate, Pul A. APPLICANT: Mannion, Jane
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
| TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER FILE REFERENCE: 210121.590
| CURRENT FILING DATE: 2002-10-02
| NUMBER OF SEQ ID NOS: 111
| SOFTWARE: COTIXA INVENTION Disclosure Database
| SEQ ID NO 90
| LENGTH: 253
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                                                                                                          CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIPICATION: <UNknown>
                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/210,084
FILING DATE: CUNKINOM:
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                           OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diske
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Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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tes 9, Conserv
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US-09-905-083-33
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APPLICANT: Ginberg, Wendy M.
APPLICANT: Ginberg, Wendy M.
APPLICANT: Ginberg, Wendy M.
APPLICANT: Ginberg, Wendy M.
APPLICANT: Ginberg, Wichard
APPLICANT: Ginberg, Nate C.
APPLICANT: Ginberg, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Mursay, Richard
APPLICANT: Mothods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: MOTHORE: 10/3/0/25,027
CURRENT APPLICATION NUMBER: US 60/35,037
CURRENT FILING DATE: 2000-0-1-1-3
PRIOR FILING DATE: 2001-11-1-3
PRIOR APPLICATION NUMBER: US 60/336,34
PRIOR FILING DATE: 2001-11-29
PRIOR PRILING DATE: 2002-01-10
PRIOR PRIPARE PRIOR PRILING DATE: 2002-01-10
PRIOR PRIPARE PRIPARE PRIPARE PRIPARE PRIPARE PRIPARE PRI
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Sequence 48, Application US/10173999
Publication No. US20040005563A1
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Gish, Kurt C.
TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions TITLE OF INVENTION: Methods of Screening for Modulators of Ovarian TITLE OF INVENTION: Cancer FILE REFERENCE: 018501-002420US
CURRENT APPLICATION NUMBER: US/10/173,999
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/299,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                          Sequence 498, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
                                                                                                                                                                    APPLICANT: Afar, Daniel
APPLICANT: Afaz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
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Best Local Similarity 100.
Matches 9; Conservative
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3-10-295-027-498
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Patent No. US20020146708A1

Patent No. US20020146708A1

Patent No. US20020146708A1

TITLE OF INVENTION:
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer FILE REPERBURE: D62230IP/C/D13

PRIOR PILING DATE: 2001-07-13

PRIOR PILING DATE: 2001-07-13

PRIOR FILING DATE: 2000-02-11

SEQ ID NO 33

LENGTH: 9
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APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE ON Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 136
LENGTH: 9
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NAME/KRY: CHAIN
CHER INCRMATION: Residues 5-13 of the SCCE protein US-09-918-243-33
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/315,287
PRIOR PILING DATE: 2001-08-27
PRIOR PILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 48
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-918-243-33
; Sequence 33, Application US/09918243
; Patent No. US20020142317A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Gaps
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Pred. No. 12;
2; Mismatches 0; Indels
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IN BRAIN, SIGNAL = 1.5
IN PLACENTR, SIGNAL = 1.8
IN ADULT LIVER, SIGNAL = 1.6
            PRIOR AFFLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/0060
PRIOR APPLICATION NUMBER: PCT/USO1/0060
PRIOR APPLICATION NUMBER: DCT/USO1/0060
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ 1D NOS: 49117
SOFTWARE: APPLICATION NUMBER: US 09/774,203
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ 1D NOS: 49117
SOFTWARE: APPLICATION NUMBER: US 09/774,203
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ 1D NOS: 49117
SEQ 1D NO 46097
LENGTA: 23
TYPE: PRT
COTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

OTHER PROPERTION OF STATEMENT OF STATEME
PCT/US01/00666
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Best Local Similarity 77.8
Matches 7; Conservative
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US-09-895-913A-92
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Sequence '46097, Application US/09864761

GENERAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILL REPERBORE: 2001-05-23

PRICR FILING DATE: 2000-08-03

PRICR FILING DATE: 2000-08-03

PRICR FILING DATE: 2000-08-03

PRICR FILING DATE: 2000-10-04

PRICR FILING DATE: 2000-10-04

PRICR FILING DATE: 2000-08-03

PRICR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESULT 10

Sequence 10255, Application US/10369493
Sequence 10255, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Gao. Yongwei
APPLICANT: Glater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Bar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                               Query Match

90.0%; Score 36; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 5-13 of the SCCE protein 5-09-905-083-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Cytophaga hutchinsonii IS-10-369-493-10255
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0
                                                                                                   87.5%; Score 35; DB 9; Length 480;
88.9%; Pred. No. 2.6e+02;
vative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: 110 Human Secreted Proteins
FILLE REFERENCE: PZ021P1

CURRENT APPLICATION NUMBER: US/10/097,065

CURRENT FILING DATE: 2002-03-14

PRIOR FILING DATE: 1998-12-17

PRIOR FILING DATE: 1998-12-18

PRIOR FILING DATE: 1997-12-18

PRIOR FILING DATE: 1997-12-18

PRIOR FILING DATE: 1997-12-18

PRIOR FILING DATE: 1997-12-18

PRIOR PELICATION NUMBER: 60/068,057

PRIOR FILING DATE: 1997-12-19

PRIOR PELICATION NUMBER: 60/068,369

PRIOR PILING DATE: 1997-12-19

PRIOR PILING DATE: 1997-12-18

PRIOR PILING DATE: 1997-12-18
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... OTHER INFORMATION: Xaa equals stop translation US-10-097-065-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 220, Application US/10097065
Publication No. US20030055236A1
GENERAL INFORMATION:
ORGANISM: Helicobacter pylori
S-09-895-913A-92
                                                                                           Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                              238 LLPLSILL 246
                                                                                                                                                                                                                                       1 LLPLQILLL 9
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ORGANISM: Homo sapiens
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RESULT 14 US-09-933-767-1083

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Sequence 103, Application US/0933767

Publication No. US20030181692A1

APPLICAMT. Ni et al.

THILE OF INVENTION: 2001-06-22

CURRENT MI et al.

FILLE OF INVENTION: 2001-06-21

PRIOR PELICATION NUMBER: 105/09/933,767

CURRENT APPLICATION NUMBER: 105/09/933,767

CURRENT APPLICATION NUMBER: 105/09/933,767

PRIOR FILLING DATE: 2001-06-22

PRIOR PELICATION NUMBER: 60/14,36

PRIOR PELICATION NUMBER: 60/10-3,170

PRIOR PELICATION NUMBER: 60/10-3,170

PRIOR PELICATION NUMBER: 60/04,36

PRIOR PELICATION NUMBER: 60/04,365

PRIOR PELICATION NUMBER: 60/04,365

PRIOR PELICATION NUMBER: 60/04,375

PRIOR PELICATION NUMBER: 60/04,376

PRIOR PELICATION NUMBER: 60/04,377

PRIOR PELICATION NUMBER: 60/04,377

PRIOR PELICATION NUMBER: 60/04,377

PRIOR PELICATIO
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CURRENT FILING DATE: 2001.12-20

EARLIER PILING DATE: 1998-12-04

EARLIER PILING DATE: 1998-12-04

EARLIER PILING DATE: 1998-12-04

EARLIER PILING DATE: 1998-06-04

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER APPLICATION NUMBER: 60/049,881

EARLIER APPLICATION NUMBER: 60/049,881

EARLIER PILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,976

EARLIER APPLICATION NUMBER: 60/049,995

EARLIER APPLICATION NUMBER: 60/049,995

EARLIER PILING DATE: 1997-06-06

EARLIER PI
                                             APPLICATION NUMBER: US/10/023,282
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LOCATION: (8)
CTHER INNERWATION: Xaa equals any of the naturally occurring L-amino acids
S-09-933-767-1083
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Publication No. US20030092893A1
GENERAL INFORMATION:
APPLICANT: Young et al.
IIILE OF INVENTION: 207 Human Secreted Proteins
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PRIOR FILING DATE: 1997-06-06
PRIOR PELING DATE: 1997-06-06
PRIOR PELING DATE: 1997-06-06
PRIOR PELING DATE: 1997-06-06
PRIOR PELING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-06
PRIOR PELING DATE: 1997-12-18
PRIOR PELING DATE: 1997-12-18
PRIOR PELING DATE: 1997-12-18
PRIOR PELING DATE: 1997-12-18
PRIOR PELING DATE: 1998-01-30
PRIOR PELING DATE: 1998-05-18
PRIOR PELING DATE: 1998-05-19
PRIOR 
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Best Local Similarity 87.5
Matches 7; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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S-10-023-282-1083
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EARLIER APPLICATION NUMBER: 60/048,963

BARLIER FILING DATE: 1997-06-06

BARLIER FILING DATE: 1997-12-18

BARLIER FILING DATE: 1997-12-18

BARLIER FILING DATE: 1998-07-15

BARLIER APPLICATION NUMBER: 60/094,657

BARLIER FILING DATE: 1998-07-30

NUMBER OF SEQ ID NOS: 1227

BARLIER FILING DATE: 1998-07-30

NUMBER OF SEQ ID NOS: 1227

SOFTWARE: PATENTIN OF: 2.0

SEQ ID NO 1083

LENGTH: 73

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/SEX: 1898

COCATION: (8)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

S-10-023-282-1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 85.0%; Score 34; DB 14; Length 73; Best Local Similarity 87.5%; Pred. No. 59; Matches 7; Conservative 1; Mismatches 0; Indels
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earch completed: March 1, 2004, 18:08:51 ob time : 25.1111 secs

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hepatocarcinogenes
surfactant protein
conglutinin - bovi
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probable permease
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chloramphenicol re
probable transport
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stromelysin 3 (EC
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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729010 A31759 S23756 TA3366 G65039 A54984	06/314 H66811 A41720 A41927 A8334 A98157 AH1130
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## ALIGNMENTS

RESULT 1 A53968 serine proteinase SCCE precursor - human Nighternate names: stratum corneum chymotryptic enzyme (Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: O7-Jul.1995 #sequence_revision 07-Jul.1995 #text_change 22-Jun-1999 C;Species: Homo sapiens (man) C;Species: A53968 Multiple: Cloning, Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelru J; Biol. Chem. 269, 19420-19426, 1994 A;Reference number: A53968; MulD:94308225; FMID:8034709 A;Reference number: A53968; MulD:94308225; FMID:8034709 A;Residues: 1-253 <	C;Superfamily: trypsin; trypsin homology F;30-245/Domain: trypsin homology <try> Cuery Match Best Local Similarity 100.0%; Pred. No. 1.9; Length 253; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</try>
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ud, T. enzym Cation transport P-type ArPase CAC2137 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #sequence\_revision 14-Sep-2001 #sequence\_revision 14-Sep-2001 #seton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, F,Nolling, J.; Breton, G.; Omelchenko, M.V.; Smith, D.R. J. Barteriol. 183, 4823-4838, 2001 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo A;Reference number: A96900; MUID:21359325; PMID:21359325

LLPLOILLL 9

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8 8

RESULT

A)cross-references: GB:AE001437, PIDN:AAK80095.1, PID:g15025128; GSPDB:GN00168 A)Experimental source: Clostridium acetobutylicum ATCC824

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-845 <KUR>

C;Genetics: A;Gene: CAC2137

Score 36; DB 2; Length 845; Pred. No. 39; 2; Mismatches 0; Indels

90.0%;

Query Match
Best Local Similarity 77.8
Matches 7; Conservative

670 LLPIQILLI 678

1 LLPLQILLL 9

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bepatocarcinogenesis-related transcription factor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 08-Sep-1997
C;Accession: JG4857
B;Kishimoto, T.; Kokura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.
B;Cocession: JG4857
A;Title: HTP: A b-zip transcription factor that is closely related to the human XBP/TREB:
A;Reference number: JC4857
A;Reference number: JC4857
A;Residues: 1-267 «KIS>
C;Comment: This is a basic-leucine zipper type transcription factor involved in hepatocel
C;Comment: This is a basic-leucine zipper type transcription factor involved in hepatocel
C;Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C;Keywords: leucine zipper; transcription factor
F;Ss-98/Domain: fos/jun DNA-binding domain homology
F;89-126/Region: leucine zipper motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Bos primigenius taurus (cattle)
C;Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C;Accession: S33603
A;Lim, B.L.; Lu, J.; Reid, K.B.M.
Immunology 78, 159-155, 1993
A;Title: Structural similarity between bovine conglutinin and bovine lung surfactant prot A;Reference number: S33603; MUID:93170856; PMID:8436402
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000 C;Accession: UC7300
R;Masaki, T.; Noguchi, H.; Kobayashi, M.; Yoshida, M.; Takamatsu, K.
DNA Res. 7, 187-193, 2000
A;Title: Isolation and characterization of the gene encoding mouse tax-responsive element A;Reference number: UC7300
A;Accession: UC7300
A;Molecule type: mRNA
A;Residues: 1-266 <MAS>
A;Coss-references: DDBJ:AB036745
C;Genetics:
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C;Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C;Keywords: leucine zipper; transcription factor
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-369 <LIMA
C,Superfamily: pulmonary surfactant protein D, C-type lectin homology
F;248-367/Domain: C-type lectin homology <LCH>
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Pred. No. 30;
0; Mismatches
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Pred. No. 30;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.0%;
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les 8; Conserv
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Best Local Similarity
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nes 8; Conserv
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Best Local S:
Matches 8
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JC4857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: B64638
; Tomb, J.F.; Walley, C.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne on, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. ature 388, 539-547, 1997
; Althorers Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  onserved hypothetical integral membrane protein HP0946 - Helicobacter pylori (strain 26;Species: Helicobacter pylori
;Species: Helicobacter pylori
;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; nucleic acid sequence not shown; translation not shown; Molecule type: DNA; Molecule type: DNA; TOPA; Crossiques: 1.496 < TOM>; Crossiques: 1.496 < TOM>; Crossiques: CB: ABC000604; GB: ABC000511; NID: 92314086; PIDN: AAD07993.1; PID: 9231408
                                                                                                                                                                                                                                                                                                                                       Species: Helicobacter pylori
Species: Helicobacter pylori
Species: Helicobacter pylori
Variety: strain J99
Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
Accession: A71875
Accession: A71875
Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title: Genomic sequence comparison of two unrelated isolates of the human gastric path Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: DNA
|Residues: 1-493 <ARN>
|Cross-references: GB:AE001518; GB:AE001439; NID:g4155454; PIDN:AAD06464.1; PID:g415546
|Bayerimental source: strain J99
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Length 493

Score 35; DB 2; Pred. No. 36; 0; Mismatches

87.5%;

Query Match
Best Local Similarity 88.9
Matches 8; Conservative

Gene: jhp0880

Status: preliminary

Libisitii 262

1 LLPLOILLL 9

Score 35; DB 2; Length 496; Pred. No. 36; 0; Mismatches 1; Indels

87.5%;

Conservative

Query Match Best Local Similarity Matches 8; Conserv

Start codon: GTG

Genetics

|||| |||| |LPLSILLL 262

1 LLPLOILL 9

- mouse

ax-responsive element-binding protein 5; Species: Mus musculus (house mouse)

ESULT 5 C7300

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Cispecies: Bos primigentus taurus (cattle)
Cispecies: Bos primigentus taurus (cattle)
Cibate: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 20-Aug-1999
Cibate: 1277-281 1994
A; Hartshorn (BC) mRNA expressed in liver: cloning and characterization of A; Reference number: 145878
A; Reference number: 145878
A; Residues: 1-371 < LIO>
A; Residues: 1-371 < LIO>
A; Residues: 1-371 < LIO>
C; Superfamily: pulmonary surfactant protein D; C-type lectin homology
C; Superfamily: pulmonary surfactant protein D; C-type lectin homology
                                                                                                                                                                                                                                                                                                                                                                                             Antrons (57/1; 106/1; 142/1; 178/1; 245/1
C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
C;Keywords: calcium binding; glycoprotein; hydroxylvaine; hydroxyproline
F;1-20/Domain: signal sequence #status predicted <21G>
F;1-20/Domain: signal sequence #status predicted <21G>
F;21-31/Product: conglutinin #status predicted <MAI>
F;46-214/Region: collagan-like
F;548-36/Domain: C-type lectin homology <LCH>
F;248-36/Domain: C-type lectin homology <LCH>
F;63,87,99,135,141,159,162,198,210/Modified site: S-hydroxylysine (Lys) #status experimer
F;63,87,99,135,141,159,162,198,210/Modified site: S-hydroxylysine (Pro) #status experimer
F;78,56,108,111,129,132,147,153,171,195/Modified site: 4-hydroxyproline (Pro) #status experimental
Ridiou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry, J. Immunol. 153, 173-180, 1994
A; Immunol. 153, 173-180, 1994
A; Title: Bovine conglutinin gene exon structure reveals its evolutionary relationship to A; Reference number: 146010; MUID:94267222; PMID:8207234
A; Accession: 146010
A; Sature: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-371 < LIO>
                                                                                                                                                                                                                                                     Cross-references: EMBL:U06860; NID:9507183; PIDN:AAB60624.1; PID:9514256; Comment: This protein mediates the agglutination of erythrocytes with antibody and comp. Comment: This protein is a Ca2+-dependent serum lectin specific for N-acetylglucosamine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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Cibate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999
Cibate: 15-0ct-1999 #sequence_revision 15-0ct-1999
Cibacession: T17215
Ripoustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18723
A;Reference number: Z18723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 1; Length 371;
Pred. No. 42;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 371;
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Pred. No. 42;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.0%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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es 7; Conserv
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T17215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Molecule type: protein
, Residues: 21-209, 'S', 211-371 < LEE>
, Kawasaki, N.; Yokota, Y.; Kawasaki, T.
rch. Biochem. Biophys. 305, 333-540, 1993
, Thile: Differentiation of conglutination activity and sugar-binding activity of conglu; Reference number: $36879; MUID:93384312; PMID:8373191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawasaki, N.; Itoh, N.; Kawasaki, T.
lochem. Biophys. Res. Commun. 198, 597-604, 1994
Title: Gene organization and 5'-flanking region sequence of conglutinin: A C-type mamm
Reference number: JC2396; MUID:94128104; PMID:8297370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Residues: 1-371 -KADA
*Residues: 1-371 -KADA
*Note: The authors translated the codon GAT for residues 250 and 270 as Glu
*Lu, J.; Laursen, S.B.; Thiel, S.; Jensenius, J.C.; Reid, K.B.M.
*Iochem. J. 292, 157-162, 1993
*Title: The CDNA cloning of conglutinin and identification of liver as a primary site
*Reference number: $33235; MUID:93277452; PMID:7684896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee, Y.M.; Leiby, K.R.; Allar, J.; Paris, K.; Lerch, B.; Okarma, T.B.
Title: Primary structure of bovine conglutinin, a member of the C-type animal lectin Reference number: A23740; MUID:91131556; PMID:1993651
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Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
Accession: JN0450; JC2396; S33235; A33740; S36879; S35044; I46010; A29416; S34054
Suzuki, Y.; Yin, Y.p.; Makino, M.; Kurimura, T.; Wakamiya, N.
Cochem. Biophys. Res. Commun. 191, 335-342, 1993
Title: Cloning and sequencing of a cDNA coding for bovine conglutinin.
Reference number: JN0450; MUID:93213261; PMID:8460993
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Residues: 1-172, H',174-217, A',219-271,'V',273-371 <LUU>
(Cross-references: EMBL:X71774; NID:g395267; PIDN:CAA50665.1; PID:g395268
EXPERIMENTAL SOURCE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: DDBJ:D14085; NID:g285643; PIDN:BAA03170.1; PID:g285644
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      Gaps
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Residues: 75-86, X', 88-89, X', 91,'I' <LUA>

Experimental source: lung

Young, N.M.; Leon, M.A.

Young, N.M.; Leon, M.A.

Young, The carbohydrae specificity of conglutinin and its

Reference number: A29416; MUD:87184551; PMID:3566740
      Indels
      ä
      Mismatches
                                                                                                                                                                                                                                                                                                      names: C3b-binding protein conglutinin-N
      ä
         Conservative
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Residues: 1-371 <SUZ>
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      7;
                                                                                                                                                                                                                                                                                                                   Alternate
            Matches
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Status: preliminary

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Cjaccession: H84314
Rjug W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
Ajatuhors: Hou, S.; Daniells, C.J.; Dennis, P.P.; Once, R.D.; Ebhardt, H.; Lowe, T.M.; Liê, Ajatuhors: Hou, S.; Daniells, C.J.; Dennis, P.P.; Once, R.D.; Ebhardt, H.; Lowe, T.M.; Liê, Ajatiel: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CiSpecies: Pyrococcus abyssi
CiSpecies: Pyrococcus abyssi
CiDate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 08-Sep-2000
CiAccession: H75201
R;anonymous, Genoscope
R;anonymous, Genoscope
A;bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struct.
A;Reference number: A75001
                                                                                                                                                                      C)Accession: T50904

R;Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.

B;Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.

B;Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.

B;Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynt;

A;Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynt;

A;Accession: T50904

A;Accession: T50904

A;Accession: P50904

A;Retus: preliminary; translated from GB/EMBL/DDBJ

A;Retus: preliminary; translated from GB/EMBL/DDBJ

A;Retus: preliminary; translated from GB/EMBL/DDBJ

A;Retus: preliminary; Lanslated from GB/EMBL/DDBJ

A;Retus: preliminary; Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase

C;Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: GB:AJ248283; GB:AL096836; NID:95457433; PIDN:CAB49063.1; PID:el51495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytochrome aa3 controlling protein [imported] - Halobacterium sp. NRC-1
C.Species: Halobacterium sp. NRC-1
C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                        Mg protoporphyrin methyl transferase [imported] - Rubrivivax gelatinosus C;Species: Rubrivivax gelatinosus C;Species: Rubrivivax gelatinosus C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #sequenge 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.5%; Score 33; DB 2; Length 146; 66.7%; Pred. No. 26; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein PAB0088 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.0%; Score 34; DB 2; Length 123 ilarity 88.9%; Pred. No. 1.48+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C, Superfamily: Pyrococcus abyssi hypothetical protein PAB0088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Experimental source: strain Orsay
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LLPLQIIIV 76
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Matches 6; Conserv
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ses 8; Conserv
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Molecule type: DNA
Residues: 1-146 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: H75201
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A;Gene: PAB0088
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Best Local S
Matches 8
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1, Molecule type: DNA
1, Molecule type: DNA
1, Fassiduss: 1-539 < STO.
1, Cross-references: GB:AE004934; GB:AE004091; NID:G9951515; PIDN:AAG08601.1; GSPDB:GN001
1, Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               obable permease of ABC iron transporter PA5216 [imported] - Pseudomonas aeruginosa (sd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: H82994

Stower, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
distant, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.

ature 406, 959-964, 2000

inture 406, 959-964, 2000

'Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patholyTitle: Complete genome PA01, PMID:20437337; PMID:10984043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Pseudomonas aeruginosa
Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 2; Length 539;
Pred. No. 62;
1; Mismatches 1; Indels
                                                                                                                                                                                                                           Length 429
,Molecule type: mRNA
|Residues: 1-429 <POU>
|Cross-references: EMBL:AL117404
| Cross-references: EMBL:AL117404
| Genetics: Adult testis; clone DKFZp434H2235
|Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Cross-references: EMBL:AL080133
A.Experimental source: adult testis; clone DKFZp434G173
                                                                                                                                                                                                                    85.0%; Score 34; DB 2;
87.5%; Pred. No. 49;
live 1; Mismatches
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                                                                                                                                                                                                                           Query Match
Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Superfamily: sfuB protein
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                                                                                                                                                                                                                                                                                                                                                                                                 381 LPLQLLL 388
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A, Molecule type: mRNA
A, Residues: 1-1092 < WAM>
                                                                                                                                                                                                                                                                                                                                                              2 LPLQILLL 9
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                                                                                                                                                               Note: DKFZp434H2235.1
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Gaps

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Wed Mar 3 07:49:14 2004
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;Accession: H84314
;Status: preliminary
;Molecule type: DNA
;Residues: 1.277 <STO>
;Cross_references: GB:AE004437; NID:g10581096; PIDN:AAG19884.1; GSPDB:GN00138
;Genetics:
                                                                                                                                                                                                           Query Match
82.5%; Score 33; DB 2; Length 277;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 0; Indels
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0; Gaps

earch completed: March 1, 2004, 17:36:30 ob time: 12.3333 secs

1 LLPLOILL 8 |||||::| 98 LLPLOVIL 105

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

1 protein - protein search, using sw model

In on: March 1, 2004, 17:17:25 ; (without alignments)

78.105 Million cell updates/sec
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itle:

WS-09-905-083-35

erfect score: 40

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eriect score: 40
equence: 1 LLPLQILLL 9
coring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

earched: 141681 seqs, 52070155 residues

otal number of hits satisfying chosen parameters: 141681

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latabase : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	P49862 homo B	Q9d1m7 mus musculu	077755 trichosurus	P35246 bos taurus	Q8mhz9 bos taurus	P23805 bos taurus	homo		homo	vibri	homod	homod	mus r			esch	homo	MUS	homod	P12821 homo sapien	xenot	Q8k1m5 rattus norv		homo	Q9jmg3 mus musculu		P42916 bos taurus	rattı	P18065 homo sapien	eache	318 homo	43 homo	n aum 703
SUMMARIES	ΠD	_	FK11 MOUSE	IHA TRIVU	PSPD_BOVIN	CL46_BOVIN		SNE2_HUMAN	SNE1_HUMAN	FK11_HUMAN	TOXR_VIBCH	YA06_HUMAN	YA04_HUMAN	APP1 MOUSE	MCT1 PAPHA	LPSB_PERAM	ARAJECOLI	SEPL HUMAN	MM11_MOUSE	MM17 HUMAN	ACE HUMAN	CFTR_XENLA	NPW_RAT	EFA2 MOUSE	EFA2_HUMAN	CG21_MOUSE	CG21_HUMAN	CL43_BOVIN	PPAS_RAT	IBP2_HUMAN	YFUD_ECOLI		HRA1_HUMAN	PVR2_MOUSE
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æ	Query Match	100.0	95.0	95.0	85.0	85.0	85.0	85.0	85.0	82.5	82.5	82.5	82.5	82.5	90.08	80.0	80.0	80.0	80.0	80.0	80.0	80.0	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5
	Score	40	38	38	34	34	34	34	34	93	33	33	. 33	33	32	32	32	32	32	32	32	32	31	31	31	31	31	31	31	31	31	31	31	31
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APP1 HUMAN NX2B_HUMAN PTPE HUMAN PTPE HUMAN CHC2 HUMAN CLR2_MOUSE PC16 HUMAN PC16 HUMAN PC16 HUMAN RC16 HUMAN RC16 BOVIN YCBC_ECOLI	
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77.75 77.77 77.75 77.75 77.75 77.75 77.75 77.75	

## ALIGNMENTS

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cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines. -!- TISSUE SPECIPICITY: Abundantly expressed in the skin and is expressed by kerathocytes in the epidermis. Very low levels are also seen in the brain and kidney. -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.

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N-LINKED (GLCNAC. . .) (POTENTIAL). ACTIVATION PEPTIDE. KALLIKREIN 7. 27525 MW; 246 2 253 AA; ACT SITE ACT SITE ACT SITE DISULFID DISULFID DISULFID SEQUENCE DISULFID PROPEP  $\Sigma$ 

Query Match

Query Match

100.0%; Score 40; DB 1; Length 253;
Best Local Similarity 100.0%; Pred; No. 1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Mismatches 0; Indels

. 0

Mus musculus (Mouse)

PRII MOUSE STANDARD, PRT; 201 AA.
Q9DIMT; OQCRE4;
28-FEB-2003 (Rel. 41, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
FKSG6 binding protein 11 precursor (RC 5.2.1.8) (Peptidyl-prolyl cistrans isomerase) (PPIase) (Rotamase) (19 kDa FKSG6-binding protein) FKBP11. FXII MOUSE ID FXII MO AC Q9DIM/I OT 28-FEB-OT 28-FEB-OT 15-MAR-DE TEARS I DE TEARS I DE FEBE-DE FEBE-

Mandon M. Ishing Y., Shibadaw A., Shibada K., Yoshino M., Itoh M., Ishin Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Adachi Y., Gojobori T., Riyosawa H., Kondo S., Yamanaka I., Asito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsud H.A., Ashburner M., Batalov S., Casavant T., Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Brownstein M.J., Mashima J., Maszarelli J., Mombaers P., Narchionni L., Mashima J., Mazzarelli J., Mombaers P., Narchionni L., Mashima J., Mazzarelli J., Mombaers C., Ringawal M., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Sazaki H., Toyo-oka K., Mang K.H., Weitz C., Milttaker C., Willatha L., Mayshima Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., M. Hartional annotation of a full-length mouse cDNA collection."; Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI\_TaxID=10090; STRAIN=C57BL/6J, TISSUE=Embryo; MEDLINE=21085660; PubMed=11217851; SEQUENCE FROM N.A. 

RECOURTE FROM N.A.

REC STRAINE-278B/637 TISSUE-Mammary gland;

REC MEDLINE-22386257, Pubmed-12477932,

RECOURTE FROM N.A.

STRAINE-22386257, Pubmed-12477932,

RECOURTE R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Babt N.R.,

RICHORNE R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Frange C.,

RA Brownstein M.J., Waldin T.B., Toshlyuki S., Carninci P., Frange C.,

RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raba S.S., Moran P.J., McKernan K.J., Malek J.A., Gunsarene P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

ROHINGTON: Political analysis of more than 15,000 full-length

R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC II- FUNCTION: Petrase accelerate the folding of proteins during protein synthesis.
-!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline

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HSSP, P20071; IFKJ. MGD; MGI.1913370; FKbpll. MICEPPO; IPRO01179; FKBP\_PPIASE. PEAM; PP00254; FKBP; I. PROSITE; PS00453; FKBP\_PPIASE\_1; 1. EMBL; AK003331; BAB22719.1; -. EMBL; AK019132; BAB31559.1; -. EMBL; BC037596; AAH37596.1; -.

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J. MOI. Endecrinol. 21:141-152 (1998).

J. MOI. Endecrinol. 21:141-152 (1998).

RESPECTIVEN: THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

INHIBINS/ACTIVENS. THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

INHIBINS/ACTIVENS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHAMIC AND PITUITARY HORMONE SECRETION, GRANDAL HORMONE SECRETION, GRAN CELL DEVELOPMENT AND MATURATION, EXTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL, EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR SUBJURIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=99027340; Pubmed=9801457;
Vanmontfort D., Fidler A.E., Heath D.A., Lawrence S.B., Tisdall D.J.,
Greenwood P.J., McNatty K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "CDNA sequence analysis, gene expression and protein localisation of
the inhibin alpha subunit of Australian brushtail possum (Trichosurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trichosurus vulpecula (Brush-tailed possum).
Bukaryota, Metazoa, Chordata, Craniata, Verrebrata, Buteleostomí,
Mammalia, Metatheria, Diprotodontia, Phalangeridae, Trichosurus.
VCEL_TaxID=9337;
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INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
-i- SIMILARITY: Belongs to the TG-beta family.
                                                                                                                                     28 201 FK506 BINDING PROTEIN 11.
57 144 PPIASE, FKBP-TYPE
53 53 -> F (IN REP. 1; BAB31559).
198 198 -> R (IN REP. 1; BAB31559).
201 AA, 22137 WW, 94D955C57264BD82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    95.0%; Score 38; DB 1; Length 201; 88.9%; Pred. No. 2.1; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AF033340, AAC63945.1; -. 60, 00005576; Cextracellular, ISS. 60, G0:0005576; Cextracellular, ISS. 60, G0:0005125; F:activin inhibitor activity; ISS. 60, G0:0005125; F:cytokine activity; ISS. 60, G0:0003793; F:cdfense/immunity protein activity; ISS. 60, G0:0005179; F:protein binding; ISS. 60, G0:0005179; F:protein binding; ISS. 60, G0:0005515; P:protein binding; ISS. 60, G0:0005516; P:protein binding; ISS. 60, G0:0005169; P:protein binding; ISS. 60, G0:0005169; P:protein differentiation; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 361 AA.
PROSITE; PS00454; FKBP_PPIASE_2; FALSE_NEG.
PROSITE; PS50059; FKBP_PPIASE_3; 1.
ISOMETASE; Rotamase; Signal. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inhibin alpha chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
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Best Local Similarity
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077755;
                                                                                                                                                  CHAIN
DOMAIN
CONFLICT
CONFLICT
SEQUENCE
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LIAIM OF THAM 
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DR GO; GO:0008151; P:cell growth and/or maintenance; ISS.

GO; GO:0007166; P:cell gurface receptor linked signal transdu. ., ISS.

BR GO; GO:0007267; P:cell-cell signaling; ISS.

BR GO; GO:0004254; P:erell-cell signaling; ISS.

DR GO; GO:004254; P:hemoglobin biosynthesis; ISS.

GO; GO:0045578; P:hemoglobin biosynthesis; ISS.

BR GO; GO:0045578; P:hemoglobin biosynthesis; ISS.

GO; GO:0045578; P:hemogliber requilation of B-cell differentiation; ISS.

BR GO; GO:0045578; P:hemoglive requilation of follicle-stimulating. .; ISS.

GO; GO:0045679; P:hemoglive requilation of interferor-gamma bio. .; ISS.

GO; GO:0045560; P:negative requilation of follicle-stimulating. .; ISS.

GO; GO:0045650; P:negative regulation of phosphorylation; ISS.

GO; GO:0046881; P:positive regulation of follicle-stimulating. .; ISS.

InterPro; IPR00189; TGFb.

PR PRINTS; PR00669; INHIBINA.

PR PROSITE; PS00250; TGF BETA 1: 1.

PR PROSITE; PS00250; TGF BETA 1: 1.

PROSITE; PS00250; TGF BETA 1: 1.

POWNETTAIL.

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POWNETTAIL I PROFILED.

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PROSITE; PS00250; TGF BETA 1: 1.

POWNETTAIL I PROFILED.

PROSITE; PS00250; TGF BETA 1: 1.

PROFILED.

PR
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"Structural similarity between bovine conglutinin and bovine lung surfactant protein D and demonstration of liver as a site of surfactant protein D and demonstration of liver as a site of surfactant protein D and demonstration of liver as a site of surfactant protein D and demonstration of liver as a site of Immunology 78:159-165(1993).

-!-PUNCTION: Contributes to the lung's defense against inhaled microorganisms. Binds strongly malcose residues and to a lesser extracellular reorganization or tunnover of pulmonary surfactant.
-!-SUBJMIT: Oligomeric complex of 4 set of homotrimers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.

BY SIMILARITY.

N-LINKED (GLCNAC. ...) (POTENTIAL).

N-LINKED (GLCNAC. ...) (POTENTIAL).
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1-FEB-1994 (Rel. 28, Last sequence update)
15-ULI-1999 (Rel. 38, Last amnotation update)
Pulmonary surfactant-associated protein D precursor (SP-D) (PSP-D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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Pred. No. 3.6;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D661CDF93CDAA87D CRC64;
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MEDLINE=93170856; PubMed=8436402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 230 BY
251 361 INI
260 323 361 ENY
289 358 BY
293 360 INY
322 360 INY
48 48 N-I
144 144 N-I
266 266 N-I
361 AA, 38945 MW, I
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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PSPD BOVIN
ID PSPD BOVIN
AC P35246;
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DISULFID
DISULFID
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SUBUNIT: Oligomeric complex of 4 set of homotrimers (By

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Protein There are 4 surfactant consists of 90% lipid and 10% protein. There are 4 surfactant-associated protein: 2 collagenous, carbodydrate-binding glycoproteins (SP-B and SP-D) and 2 small hydrophobic proteins (SP-B and SP-C).

1- SIMILARITY: Contains 1 collagenous domain.

1- SIMILARITY: Contains 1 c-type lectin family domain.

1- SIMILARITY: Contains 1 c-type lectin family domain.

1- SIMILARITY: Contains 2 c-type lectin family domain.

1- SIMILARITY: Contains 3 c-type lectin family domain.

1- SIMILARITY: Contains 3 c-type lectin family domain.

1- SIMILARITY: Contains 1 c-type lectin family domain.

1- SIMILARITY: Contains 1 c-type lectin family domain.

1- SIMILARITY: Contains 2 c-type lectin family domain.

1- SIMILARITY: Contains 3 c-type lectin family as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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HSSP; P3547; 1B08.
Interpro; 1PR008160; Collagen.
Interpro; 1PR008160; Collagen.
Pf P800819; CLECT, C.
PREMI, PF00199; CLECT, C.
PROSTITS; P8000619; CTYPE LECTIN 1; 1.
PROSTITS; P8000619; CTYPE LECTIN 2; 1.
Glycoprotein; Calcium; Surface Film; Gaseous exchange; Hydroxylation; Signal; Lectin; Collagen; Repeat; Colled coil.
Signal; Lectin; Collagen; Repat; Coiled coil.
CHAIN
21 369 PULMONARY SURFACTANT-ASSOCIATED PROPEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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SEQUENCE FROM N.A.
Skjoedt K., Holm D., Moeller V., Vitved L., Bendixen C., Reid K.B.M.,
Skjoedt K., Holmskov U.;
"CL-46, a novel collectin highly expressed in the bovine thymus and
liver.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Ammaalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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COLLED COLL (POTENTIAL).

COLLED COLL (SHORT FORM).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINESD GECORC. ..) (POTENTIAL HYDROXYLATION (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07D88B24E0AEB2E3 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Collectin-46 precursor (CL-46) (46 kDa collectin).
CL46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 371 AA.
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Q8MHZ9;
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DISULFID
DISULFID
CARBOHYD
MOD RES
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1146 BOVIN
1146 BOVIN
1246 BOX
128-FEB-
137 28-FEB-
138-FEB-
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

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Lu J., Laursen S.B., Thiel S., Jensenius J.C., Reid B.M.;
"The cDNA cloning of conglutinin and identification of liver as a
primary site of synthesis of conglutinin in members of the Bovidae.";
Biochem. J. 292:157-162(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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Suzuki Y. Yin Y. Makino M., Kurimura T., Wakamiya N.;
"Cloning and sequencing of a cDNA coding for bovine conglutinin.";
Biochem. Biophys. Res. Commun. 191:335-342(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF509589; AAM34742.1; -
EMBL; AF509590; AAM34742.1; -
InterPro; IPR001160; Collagen.
InterPro; IPR001304; Lectin_C.
Fram; PF001391; Collagen; 2;
Pfam; PF00059; lectin_C;
PROSITE; R00004; CLECT; 1.
PROSITE; PS50041; C_TYPE LECTIN 1; 1.
PROSITE; PS50041; C_TYPE LECTIN 2; 1.
Lectin; Hydroxylation; Glycoprofein; Mannose-binding; Membrane;
Collagen; Repeat; Calcium; Signal.
SIGNAL.
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BY SIMILARITY.

N-LINKED (GLCMAC. ) (FOTENTIAL)

108AC45A91420E83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-TYPE LECTIN (SHORT FORM).
CELL ATTACHMENT SITE (POTENTIAL).
                       85.0%; Score 34; DB 1; Length 371; 77.8%; Pred. No. 23; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONG_BOVIN STANDARD; FRT; 371 AA. P23805; 097748; 01-NOV-1991 [Rel. 20, Created) 01-FBE-1994 [Rel. 28, Last sequence update) 01-OCT-1996 [Rel. 34, Last annotation update) Conglutinin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLLECTIN-46.
COLLAGEN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 371 C-:
201 203 CBI
275 369 BY
347 361 BY
90 90 N-:
371 AA, 37445 MW,
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY SEQUENCE OF 21-52.
MEDLINE=87184551; PubMed=3566740;
Young N.M., Leon M.A.;
Theo marbohydrate specificity of conglutinin and its homology to proteins in the hepatic lectin family.";
Biochem. Biophys. Res. Commun. 143:645-651(1987).
-: FUNCTION: Calcium-dependent lectin-like protein which binds to a yeast cell wall extract and immune complexes through the complement component (C3bi). It is capable of binding nonreducing terminal N accetylglucosamine, mannose, and fucose residues.
-: SUBUNIT: Oligomeric complex of 4 set of homotrimers.
-: SIMILARITY: Contains 1 collagenous domain.
                                 TISSUB=Liver;
MEDLINE=94215917; PubMed=8163202;
Liou L.S., Sastry R., Hartshorn K.L., Lee Y.M., Okarma T.B.,
Liou L.S., Sastry K.N.;
"Auber A.I., Sastry K.N.;
"Bovine conglutinin (BC) mRNA expressed in liver: cloning and
characterization of the BC cDNA reveals strong homology to surfactant
                                                                                                                                                                                                                                                                                                                                                                    AEDDINE-54128104; PubMed-8297370; Kawasaki N., Itch N., Kawasaki T.; "Gene organization and 5'-flanking region sequence of conglutinin: a C-type mammalian lectin containing a collagen-like domain."; Biochem. Biophys. Res. Commun. 198:597-604(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 21-371.
MEDILIE-91131556; Pubmed=1993651;
MEDILIE-91131556; Pubmed=1993651;
Lee Y.-M., Leiby K.M., Allar J., Paris K., Lerch B., Okarma T.B.;
"Primary structure of bovine conglutinin, a member of the C-type
                                                                                                                                                                                                                    MEDLINE=94267222; PubMed=8207234;
Liou L.S., Sastry R., Hartshorn K.L., Lee Y.M., Okarma T.B.,
Tauber A.I., Sastry K.N.;
"Bovine conglutinin gene exon structure reveals its evolutionary
relationship to surfactant protein-D.";
J. Immunol. 153:173-180(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                animal lectin family.";
J. Biol. Chem. 266:2715-2723(1991);
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U06855; AAB60624.1; JOINED.
U06856; AAB60624.1; JOINED.
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EMBL, X71774; CAA5065.1; --
EMBL; L18871; AAA20126.1; --
EMBL; U06860; AAB60624.1; --
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AAB60624.1;
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                                                                                                                                     protein-D.";
Gene 141:277-281(1994).
[3]
SEQUENCE FROM N.A.
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EMBL;
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    SEQUENCE FROM N.A. (ISOFORMS 1 AND 9), FUNCTION, CHARACTERIZATION, AND

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GWXH0; OSNIX3; QBNY49; QSTER?; Q8WWW3; Q8WWW5; Q8WXH1;
Q9NU50; Q9UFQ4; Q9YZL4; Q9YQR1;
10-OCT-2003 [Rel. 42, Lest sequence update)
10-OCT-2003 [Rel. 42, Lest sequence update)
10-OCT-2003 [Rel. 42, Lest annotation update)
Nesprin 2 (Nuclear envelope spectrin repeat protein 2) (Syme-2)
Nesprin (Symaptic nuclear envelope protein 2) (Nucleus and actin connecting element protein) (NUANCE protein).
SYNEZ OR NUA OR KIRA1011.
RMBL; D25301; BAA04983.2; JOINED.
R PIR; 145878; 145878
R PIR; J046490; J04650.
R HSSP; P35447; LB08.
R InterPro; IPR00161; Collagen.
R InterPro; IPR00160; Collagen.
R InterPro; IPR001304; Lectin.
R Ffam; PF00059; lectin.
R Pfam; PF00059; lectin.
R PFAMF; SMO00007; C1g_helix; l.
R PROSITE; PS00641; CIPPE_LECTIN 1; l.
R PROSITE; PS00641; CIPPE_LECTIN 2; l.
M Collagen; Repeat; Calcium; Signal.
I 20
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
CELL ATTACHENT SITE (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
R -> H (IN REF. 2 AND 3).
K -> S (IN REF. 2 AND 3).
V -> A (IN REF. 2).
V -> A (IN REF. 2).
V -> A (IN REF. 2).
W -> B -> V (IN REF. 2).
W -> B -> V (IN REF. 2).
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MEDLINE-22113122; PubMed=12118075;
MEDLINE-22113122; PubMed=12118075;
MEDRY.-Y., Liborter T., Munck M., Noegel A.A., Korenbaum E.;
"NUANCE; a giant protein connecting the nucleus and actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 1; Length 371;
Pred. No. 23;
1; Mismatches 1; Indels
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C-TYPE LECTIN (SHORT FORM)
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MEDLINE=21652858; PubMed=11792814;
                                                                                                                                                                                                                                                                                                                                                                                                                      CONGLUTININ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative 1
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9311
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Heilig R., Eckeberg R., Petit J.-L., Fonknechten N., Da Silva C., A Cattolico L., Levy M., Barbe V. De Berardinis V., Ureta-Vidal A., Pelletier E., Vico V., Anthouard V., Rowen L., Madan A., Qin S., Sun H., Du H., Pepin K., Artiguaneve F., Robert C., Cruaud C., Bruels T., Jaillon O., Friedlander L., Samson G., Brottier P., Caraud C., Bruels T., Jaillon O., Friedlander L., Samson G., Brottier P., Anach N., Boscus D., Dickhoff R., Dors M., Dubois I., Friedman C., Guyvenoux M., James R., Madan A., Mairey-Estrada B., Mangenot S., Martins N., Menard M., Oztas S., Ratcliffe A., Shaffer T., Trask B., A Wacherie B., Bellemere C., Belser C., Besnard-Gonnet M., Vacherie B., Bellemere C., Besnard-Gonnet M., Bartol-Mavel D., Boucard M., Briez-Silla S., Combete S., Dufosse-Laurent V., Ferron C., Icchaplais C., Louesse C., Muselet D., A Magdelenat G., Pateau E., Bellet E., Sirvain-Trukniewicz P., Trybou A., Vega-Czarny N., Bataille E., Bluet E., Bordelais I., Dubois M., Nebert D., Wunderle E., Gaurpell G., Roy A., Sainte-Marthe L., Nerdier J., Welser G., Wincker P., Walcrston R., Hood L., Weissenbach J., Mincker P., Saurin W., A., When DNA sequence and analysis of human chromosome 14.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE=22388257;

MEDINE=22388257;

MEDINE=22388257;

MEDINE=22388257;

MISTORE R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D., Strausberg R.L., Feingold B.A., Grouse L., Schomen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina R.A., Rubin G.M., Hong L., Stapleton M. Saares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Stapleton M.J. Uddin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McBan F.J., McKernan K.J., Malek J.A., Gunaratne P.H., McMardan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Villaton D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Villaton D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Paheton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Muhting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Grenzetton and initial analysis of more than 15,000 full-length human
Zhang Q., Skepper J.N., Yang F., Davies J.D., Hegyi L., Roberts R.G., Weissberg P.L., Ellis J.A., Shanahan C.M.;
"Nesprins: a novel family of spectrin-repeat-containing proteins that Localize to the nuclear membrane in multiple tissues.";
J. Cell Sci. 114:4485-4498(2001).
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                                                                                                                                                                                                  MEDIJURE-22296883; Pubmed=1248964; Zhang Q., Ragnauth C., Greener M.J., Shanahan C.M., Roberts R.G.; Theng Q., Ragnauth C., Greener M.J., Shanahan C.M., Roberts R.G.; The septins are giant actin-binding proceins, orthologous to brosophila melanogaster muscle protein MSP-300."; Genomics 80:473-481(2002).
                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Testis;
Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 6).
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Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O., Ninomiya K., Wagatsuwa M., Kanda K., Kondo H., Yokoi T., Kodaira H., Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,

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WEDINES OF 5754-6885 FROM N.A.

WEDINES-21154917; PubMed=11230166;
WEDINES-21154917; PubMed=11230166;
Wemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
Ansorge W., Boecker H., Bloecker H., Bauersachs S., Blum H.,
Lauber J., Duesterhoeft A., Beyer A., Kochrer K., Strack N.,
Mewes H.-W., Otterwaelder B., Obermaler B., Tampe J., Heubner D.,
Mambutt R., Korn B., Klein M., Poustka A.;
"Towards a catalog of human genes and proteins: sequencing and
"Towards a catalog of human genes and proteins sequencing and
analysis of 500 novel complete protein coding human cDNAs.";
Genome Res. 11:422-435(2001).
-!- FUNCTION: Involved in the maintenance of nuclear organization and
structural integrity. Probable anchoring protein which theters the
nucleus to the cytoskeleton. Connects nuclei to the cytoskeleton
C. by interacting with the nuclear envelope and with F-actin in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isold=Q8WXH0-8; Sequence=VSP_007161, VSP_007162;
Note=No experimental confirmation available;
Name=9; SynonymesNUANCE-N-3;
Isold=Q8WXH0-9; Sequence=VSP_007159, VSP_007160;
-!- TISSUE SPECIFICITY: Widely expressed, with higher level in kidney,
                                                                                                                                                                                                                                              Migase T., Ishikawa K. I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 6:63-70(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T., "Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA cDNA clones.";
DNA Res. 9:99-106 (2002).
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawata-Hio Y., Saito K., Wishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note=Produced by exon skipping that results in a frameshift. No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBGNIT: Interacts with F-actin via its N-terminal domain. SUBCRILIUMAR LOCATION: Type IV membrane protein (Potential). The largest part of the protein is cytoplasmic, while its C-terminal part is associated with the nuclear envelope, most probably the outer nuclear membrane. Remains associated with the nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    me=5; Synonyme=Alpha;
IsoId=QBWXH0-5; Sequence=VSP_007157, VSP_007164, VSP_007165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSP 007165, VSP 007166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isold=Q8WXH0-7; Sequence=VSP_007154, VSP_007163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sold=Q8WXH0-2; Sequence=VSP_007164, VSP_007166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      envelope during its breakdown in mitotic cells, ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q8WXH0-6; Sequence=VSP_007158, VSP_007
Note=No experimental confirmation available;
                                                                                                                                                                                 SEQUENCE OF 5709-6885 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [sold=Q8WXH0-3; Sequence=VSP 007155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q8WXH0-4; Sequence=VSP_007156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q8WXH0-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
MEDLINE=22158633; PubMed=12168954;
                                                                                                                                                                                                                          MEDLINE=99246063; PubMed=10231032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synonyms=Gamma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synonyms=Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=7;
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RE REPRESENTE FRANKER 
                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                            SNEI HUMAN STANDARD;
PRT; 8797 AA.

ØRNF91, 094690; QBNP97; QBNCP1; GBWWW6; QBWW71; QBWXF6; Q96N17;
Q9C0A7; Q9H525; Q9H526; Q9N336; Q9N36; Q9UJ06; Q9UJ07; Q9ULF8;
110-QCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Nesprin 1 (Nuclear envelope spectrin repeat protein 1) (Synaptic nuclear envelope protein 1) (Myocyte nuclear envelope protein 1) (Myne-1) (Myne-1) (Enaptin 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTAGENESTS OF 8758-LEU--CYS-8763.

MUTAGENESTS OF 8758-LEU--CYS-8763.

TISSUE-Heart, Placenta, Skeletal muscle, Spleen, and Testis;

MEDLINE-21652889; PubMed-11792814;

Zhang Q., Skepper J.N., Yang P., Davies J.D., Hegyi i., Roberts R.G., Weissberg P.L., Ellis J.A., Shanahan C.M.;

"Nesprins: a novel family of spectrin-repeat-containing proteins that localize to the nuclear membrane in multiple tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.0%; Score 34; DB 1; Length 6885;
87.5%; Pred. No. 4e+02;
ive 1; Mismatches 0; Indels 0; Gaps
adult and fetal liver, stomach and placenta. Weakly expressed in skeletal muscle and brain. Isoform 5 is highly expressed in pancreas, skeletal muscle and heart.

DOMAIN: The Klarsicht domain mediates the nuclear envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Heart, Spleen, and Teetis;
MEDLINE=22296983; PubMed=12408964;
Zhang Q., Ragnauth C., Greener M.J., Shanahan C.M., Roberts R.G.;
"The nesprins are giant actin-binding proteins, orthologous to
Drosophila melanogaster muscle protein MSP-360.";
Genomics 80:473-481(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                            SEQUENCE FROM N.A. (ISOFORM 1), AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OR KIAA0796 OR KIAA1756 OR KIAA1262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF495911; AAN60443.1; -.
EMBL; AL117404; CABS5905.1; -.
EMBL; AL1152832; -; NOT ANNOTATED CDS.
EMBL; AL355094; -; NOT ANNOTATED CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell Sci. 114;44B5-449B(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF435010; AAL33547.1; -. EMBL; AF435011; AAL33548.1; -. EMBL; AY061757; AAL33800.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY061758; AAL33801.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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EMBL;
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    ≥:
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Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XIX. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 7:347-355(2000).
                                                                                                                                              "The longest isoform of enaptin/Syne-1, a nuclear envelope associated protein, binds actin cytoskeleton via the alpha-actinin-like actin-binding domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUB=Adrenal gland, and Teratocarcinoma;
Ninomiya K., Magatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
Katsuta T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
Takemoto M., Ota T., Suzuki Y., Sugano S., Nagahari K., Masuho Y.,
Nagai K., Isogai T.,
Suzuki Y., Sugano S., Nagahari K., Masuho Y.,
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=99087487; PubNed=9872452;
NGDLINE=99087487; PubNed=9872452;
NGDAGES T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XI.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
DA Res. 5:277-286(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Prediction of the coding sequences of unidentified human genes. X^{\rm V}. The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. And A. A. A. C., C. Lloyd D., Parker A., Smith M., Tracey A., Williams S., Statemer S., Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
[3] SEQUENCE FROM N.A. (ISOFORM 4), AND VARIANT GLY-8323.
Braune S., Abraham S., Padmakumar V., Tunggal B., Noegel A.A., Korenbaum E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20039619; PubMed=10574462;
Nagase T., Ishikawa K.-I., Kikuno R., Hirosawa M., Nomura N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Kidney; Goud D., Lisa G., Chu S., Winnick S., Beck K.A.; Gough L., Fan J., Lisa G., Super-1."; Golgi localization of syne-1."; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ansorge W., Wirkner U., Mewes H.-W., Weil B., Wiemann S., Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 8 AND 9).
Zhang Q., Shanahan C.M.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                    Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 4219-8797 FROM N.A. (ISOFORM 7).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 28-778 AND 2901-3476 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21082932; PubMed=11214970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 6922-8797 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for large proteins in vitro.";
DNA Res. 6:337-345(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-856 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [12]
REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohara O.;
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

-- FUNCTION: Involved in the maintenance of nuclear organization and structural innegrity. Probable anchoring protein which therers the nucleus to the cytoskeleton. Connects nuclei to the cytoskeleton by interacting with the nuclear envelope and with F-actin in the cytoplasm.

--- SUBUNIT: Interacts with MUSK, with F-actin via its N-terminal domain, and with LIMA in vitro (By similarity).

---- SUBCELLULAR LOCATION: Type IV membrane protein (Potential). The Jargest part of the protein is cytoplasmic, while its C-terminal counter nuclear membrane. In skeletal and smooth muscles, a significant amount is found in the sarcomeres.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isoid=Q@NF91-9; Sequence=VSP 007133, VSP 007143, VSP 007144;
TISSUE SPECIFICITY: Widely expressed. Highly expressed in skeletal and smooth muscles, heart, spleen, and peripheral blood
                                                                                    [13]
SEQUENCE OF 7631-8797 FROM N.A., AND CHARACTERIZATION.
BEDLINE-2165978; PubMed=11801724;
MEDLINE-2165978; PubMed=11801724;
MABLOW J.M.K., Kim M.S., Davis D.B., McNally E.M.;
Myne-1, a spectrin repeat transmembrane protein of the myocyte inner nuclear membrane, interacts with lamin A/C.";
J. Cell Sci. 115:61-70(2002).
            MEDLINE=22158633; PubMed=12168954;
Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
"Construction of expression-ready cDNA clones for KIAA genes: manual
curation of 330 KIAA cDNA clones.";
DNA Res. 9:99-106(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prediction.
CAUTION: Ref.7 (BAB71097) sequence differs from that shown due
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q8NF91-4; Sequence=VSP_007134, VSP_007139, VSP_007140, VSP_0144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAUTION: Ref.14 sequence differs from that shown due to two frameshifts in positions 8412 and 8784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=2; Synonyms=Beta;
IsoId=Q8NF91-2; Sequence=VSP_007130;
Name=3; Synonyms=Alpha;
IsoId=Q8NF91-3; Sequence=VSP_007132, VSP_007144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q8NF91-5; Sequence=VSP_007135, VSP_007136;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q8NF91-6; Sequence=VSP_007137, VSP_007138;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q8NF91-7; Sequence=VSP_007141, VSP_007142;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=8; Synonyms=Beta 2;
IsoId=Q8NF91-8; Sequence=VSP_007131;
Name=9; Synonyms=Alpha 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q8NF91-1; Sequence=Displayed;
                                                                                                                                                                                                       SEQUENCE OF 8406-8797 FROM N.A.
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   TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
FK506 binding protein 11 precursor (EC 5.2.1.8) (Peptidyl-prolyl cistrans isomerase) (PPIase) (Rotamase) (19 kDa FK506-binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 1; Length 8797;
Pred. No. 5.1e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rulten S., Kay J.E., Robinson C.;
"Identification of novel FKBP genes.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                    EMEL; AY061755; AAL33798.1; --
EMEL; AY061756; AAL33799.1; --
EMEL; AF495910; AAN06442.1; --
EMEL; AF49514; AAN03486.1; --
EMEL; AY184206; AAO27771.1; --
EMEL; AY184206; AAO27774.1; --
EMEL; AL049548; CAB55865.1; ALT_SEQ.
EMEL; AL049548; CAB55866.1; --
EMEL; AL078582; CAB57866.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL136079; ', NOT ANNOTATED CDS.
AL138832; CAC16280.1; ALT SEQ.
AL138822; CAC16281.1; ALT SEQ.
AL357081; ', NOT ANNOTATED CDS.
AL560401; ', NOT ANNOTATED CDS.
AL589963; ', NOT ANNOTATED CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8749 LPLQLLLL 8756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LPLQILLL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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FK11_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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"DNA sequence of both chromosomes of the cholera pathogen Vibrio
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MEDLINE-20406833; PubMed=10952301;
Heidelberg U.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                           protein synthesis.
-i- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=Classical 569B / ATCC 25870 / Serotype Ol;
STRAIN=Classical 569B / ATCC 25870 / Serotype Ol;
MEDLINE-81102894; PubMed=3802155;
Miller V.L., Taylor R.K., Mekalanos J.J.;
Miller v.L., Taylor R.K., Mekalanos J.J.;
"Cholera toxin transcriptional activator toxR is a transmembrane DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
  "Generation and initial analysis of more than 15,000 full-length human and mouse oDNA sequences." Proc. Natl. Acad. Sci. U. S.A. 99:16899-16903(2002).
-!- FUNCTION: PPlases accelerate the folding of proteins during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bactéria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.5%; Score 33; DB 1; Length 201; 77.8%; Pred. No. 20; tive 1; Mismatches 1; Indels
                                                                                                                                          (omega=0).
-!- SIMILARITY: Belongs to the FKBP-type PPIase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 AA; 22180 MW; 586E430B9D2DC0A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. FK506 BINDING PROTEIN 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPIASE, FKBP-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P15795; Q9KTB9; 01-APR-1990 (Rel. 14, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Cholera toxin transcriptional activator. TOXR OR VC0984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSO0453; FKBP PPIASE 1; 1.
PROSITE; PSO0454; FKBP PPIASE 2; FALSE NEG.
PROSITE; PSSO059; FKBP PPIASE 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; Q00688; 1PBK.
Genew; HGNC:18624; FKBP11.
InterPro; 1PR001179; FKBP_PPIase.
Pfam; PF00224; FKBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF238079; AAF63478.1; -. EMBL; BC027973; AAH27973.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isomerase; Rotamase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 7/....
7/. Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binding protein.";
Cell 48:271-279(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LLPLQILLL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OUTCEMBAIN K.M., Dirita V.J., Mekalanos J.J.;

"TOAR Proteins with substitutions in residues conserved with OmpR
"TOAR proteins with substitution from the cholera toxin promoter.";
J. Bacteriol. 174:6807-6814(1992).
-! FUNCTION: THIS TRANSCRIPTION ACTIVATOR CONTROLS CHOLERA TOXIN,
VIBRIO CHOLERAE. IT BINDS TO THE 5'-TTTGAT-3' TANDEMLY REPEATED
DNA SEQUENCE IN CHOLERA TOXIN PROVICER REGION. TOXS. INTERACTS WITH
THE C-TERMINAL PERIPLASMIC DOMAIN OF TOXR, STIMULATING ITS
ACTIVITY. IT ACTIVATES TRANSCRIPTION AT THE PROMOTERS FOR TCPI AND
TCPA AND THIS IS PRESUMABLY VIA FORT.
-!- STMILARITY: TO B. COLI CADC, AND TO THE C-TERMINI OF A GROUP OF
TRANSCRIPTIONAL ACTIVATORS (OMPR-LIKE PROTEINS).
                                                                                                                                                          Parsot C., Mekalanos J.J.,
"Expression of ToxR, the transcriptional activator of the virulence
factors in Vibrio cholerae, is modulated by the heat shock
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 263-294 PROM N.A.
MEDLINE=91098631; PubMed=1898871;
Dirita V.J., Mekalanos J.J.,
"Periplasmic interaction between two membrane regulatory proteins,
ToxR and ToxS, results in signal transduction and transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR001867; Trans_reg_C.
Pfam: PF00486; trans_reg_C; 1.
ProDom; PD00329; Trans_c. 1.
Transcription regulation; DNA-binding; Activator; Transmembrane;
Transcription regulation; Complete proteome.
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Pred. No. 29;
1; Mismatches 1; Indels
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294 PERIPLASMIC (POTENTIAL).
134 S -> N (IN REF. 1).
172 T -> A (IN REF. 1).
184 L -> F (IN REF. 1).
204 T -> S (IN REF. 1).
32506 MW; 15EF85EA653C373E CRC64;
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                                                                                                                                                                                                                                                                response.";
Proc. Natl. Acad. Sci. U.S.A. 87:9898-9902(1990).
                                                               SEQUENCE OF 1-11 FROM N.A.
STRAIN=El Tor E7946;
MEDLINE=91088618; PubMed=2124707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93015740; PubMed=1400230;
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EMBL; M58033; AAA27575.1; -.
EMBL; M62761; AAA63558.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M21249; AAA27549.1; -.
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77.8%;
Nature 406:477-483 (2000).
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PIR; E82257; E82257.
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184
204
294 AA;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.5%; Score 33; DB 1; Length 435; 87.5%; Pred. No. 42; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Khodes S.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databaees.
-!- SIMILARITY: Belongs to the MAPE family.
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Submitted (ARR-1999) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: Belongs to the MAPE family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grafham D.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
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435 AA; 50539 MW; 3D19443032BBB494 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical protein DJ845024.2 (Fragment)
Homo sapiens (Human)
                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                      Hypothetical protein DJ845024.5 (Fragment) Homo sapiens (Human).
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Best Local Similarity 87.55
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                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 LVPLQILL 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                        YA06 HUMAN
O60813;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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WEDLINE=22388257; PubMed=12477932;

RETAINE=22388257; PubMed=12477932;

RIAUGHER R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D., Klauener R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D., A lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hokkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K.B., Sonned M.E., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Logwellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Abramson R.D., Mullahy S.J., Mark J.A., Glubbs R.A., Willahon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Willahon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mersyan A., Young A.C., Shevchenko Y., Bouffard G.G., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Butterfield X.S.N., Krzywinski M.I., Skalska U., Smallus D.E., R. Human and M. Marna M.A., Rodriguez A.C., Schein J.S., Myers R.M., Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDITINE=96139497; PubMed=8576160;
Beher D., Hesse L., Masters C.L., Multhaup G.;
"Regulation of amyloid protein precursor (APP) binding to collagen and mapping of the binding sites on APP and collagen type I.";
J. Blol. Chem. 271;1613-1620(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of a mouse brain cDNA that encodes a protein related to the Alzheimer disease-associated amyloid beta protein precursor."; Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPI MOUSE STANDARD, PRT, bos AA.

0303157, 0204038,

01-0CT-1993 (Rel. 27, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

15-MAR-2014 (Rel. 43, Last annotation update)

Amyloid-like protein 1 precursor (APLP) (APLP-1) [Contains: C30].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MEDLINE=93066322; PubMed=1279693;
Wasco W., Bupp K., Magendantz M., Gusella J.F., Tanzi R.E.,
Solomon F.;
                                                                                                                                                                                                                                                                                                                                                                    82.5%; Score 33; DB 1; Length 500;
87.5%; Pred. No. 49;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                        500 500 500 500 500 AM; 1895CD8A8F14B7C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                    EMBL; AL022101; CAA17877.1; -. EMBL; AL049681; CAB41253.1; -.
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 87.5%
                                                                                                                                                                                           Hypothetical protein.
NON TER 1 1 1 NON_TER 500 500 SEQUENCE 500 AA; 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 LVPLQÍLL 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
APP1 MOUSE
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**MEDLINE=22113598; PubMed=12228233; Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.; Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.; Scheinfeld M.H., Ghersi E., Laky K., Fowlkes B.J., D'Adamio L.; Processing of beta-amyloid precursor-like protein-1 and -2 by gamma-seretase regulates transcription."; J. Biol. Chem. 277:44195-44201(2002).

J. Biol. Chem. 277:44195-44201(2002).

General Chem. 277:44195-44201(2002).

Gamma-secretase processed fragment, ALIDI, activates transcription activation through APBBI (Fe65) binding. Couples to JIP signal transduction through C-terminal binding. May interact with cellular G-protein signaling pathways. Can regulate neurite outgrowth through binding pathways. Can regulate neurite cutgrowth through binding to components of the extracellular matrix such as heparin and collagen.

General apoptosis (By similarity).

General apoptosis (By similarity).

General and Dabl (By similarity).

HAPKBIPI and Dabl (By similarity).

Serine phosphorylation.

General DOMAIN: The NRYS sequence motification many tyrosine-

Collocation.

General DOMAIN: The NRYS sequence motification many tyrosine-

Collocation.

Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAMMA-SECRETASE PROCESSING, INTERACTION WITH APBEL, AND MUTAGENESIS OF
                                                        MEDLINE=99389880; PubMed=10460257;
Homayouni R., Rice D.S., Sheldon M., Curran T.;
"Disabled-1 binds to the cytoplasmic domain of amyloid precursor-like
                                                                                                                                                                                                                                                             MEDLINE=21408156; PubMed=11517249; Matsuda S., Yasukawa T., Homma Y., Ito Y., Niikura T., Hiraki T., Hirai S., Ohno S., Kavakawa T., Homma Y., Ito Y., Kouyama K., Yamamoto T., Kyriakis J.M., Nishimoto I.; Kyriakis J.M., Nishimoto I.; Kyriakis J.M., Lerminal Kinase (JNK)-interacting protein-1b/islet-brain-1 scaffolds Alzheimer's amyloid precursor protein with JNK."; J. Neurosci. 21:6597-6607(2001).
                                                                                                                                                                              J. Neurosci. 19:7507-7515(1999).
                                                                                                                                                                                                                                       INTERACTION WITH MAPKSIP1
[4]
INTERACTION WITH DABI.
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phosphorylated proteins is required for the specific binding of the PID domain. However additional amino acids either N. or C. terminal to the NPXY motif are often required for complete interaction. The NPXY site is also involved in clathrin-mediated

-!- PTM: Proteclytically cleaved by caspases during neuronal apoptosis. Cleaved, in vitro, at Asp-623 by caspase-3 (By endocytosis

-!- PTM: N- and O-glycosylated.
-!- MISCELLANDOUS: Binds zinc and copper in the extracellular domain.
Zinc-binding increases heparin binding. No Cu(II) reducing activity with copper-binding.
-!- SIMILARITY: Belongs to the APP family.

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PIR; A46362; A46362.

MSSP; POSO67; IMWP.

MGD; MGI:88046; APlp1.

InterPro; IPR008155; A4\_APP.

PEam; PF02177; A4\_extra.

PRINTS; PR00203; ĀMYLOIDA4. EMBL; L04538; AAA37247.1; -. EMBL; BC021877; AAH21877.1; -. PROSITE; PS00319; A4\_EXTRA; 1 SMART;

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RA Ligo Y., Karnik S., Husain A.;

RA Ligo Y., Karnik S., Husain A.;

Ligo Y., Ranik S., For Carnik S., Husain S., Hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
CLEAVAGE (BY CASPASE-3) (BY SIMILARITY).
ENDOCYTOSIS SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
PROSITE; PS00320; A4 INTRA; 1.
Apoptosis; Endocytosīs; Cell adhesion; Coated pits; Neurone;
Heparin-binding; Metal-binding; Copper; Zinc; Signal; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                             REQUIRED FOR COPPER(II) REDUCTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Papio hamadryas (Hamadryas baboon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
Y-G: REDOCED BINDING OF APBB1.
P -> PP (IN REF. 2).
56516DC3EA40E4B0 CRC64;
                                                                                                                                                                                                                          COPPER-BINDING.
ZING-BINDING (BY SIMILARITY).
HEPARIN-BINDING (BY SIMILARITY).
HEPARIN-BINDING (BY SIMILARITY).
COLLAGEN-BINDING (BY SIMILARITY).
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AC P52195;
DT 01-0CT-1996 (Rel. 34, Last sequence update)
DT 01-0CT-1996 (Rel. 41, Last annotation update)
DD Chymase precursor (EC 3.4.21.39) (Mast cell protease I).
                                                                                                               AMYLOID-LIKE PROTEIN 1.
C30 (BY SIMILARITY).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                              POTENTIAL
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NCBI_TaxID=9557;
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633
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                                                                     Glycoprotein.
SIGNAL
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TRANSMEM
DOMAIN
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MUTAGEN
CONFLICT
SEQUENCE
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SWISS-PROT entry is copyright. It is produced through a collaboration
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-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Hemolymph.
-!- INDUCTION: By introduction of foreign cells into the abdominal
--- INDUCTION: By introduction of foreign cells into the abdominal
--- INDUCTION: By introduction of foreign cells into the abdominal
--- INDUCTION: Calcium is required for lipopolysaccharide binding.
--- SIMILARITY: Contains 1 C-type lectin family domain.
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-!- FUNCTION: Participates probably in the elimination of foreign elbstances invading the insect abdominal cavity, and in trapping intracellular symbionts, when they leak from the mycetomes into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESCUENCE FROM N.A., AND PARTIAL SEQUENCE.

TISSUE-Hemolymph;
MEDILINE-91302364; pubMed=1712779;
MEDILINE-91302364; pubMed=1712779;

MEDILINE-91302364; pubMed=1712779;

"Molecular cloning of cDNA for lipopolysaccharide-binding protein from the hemolymph of the American cockroach, Periplaneta americana expression.";
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01-MAY-1992 (Rel. 22, Last sequence update)
15-MAY-1992 (Rel. 22, Last sequence update)
15-MAY-1992 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
16-MAR-2004 (Rel. 43, Last annotation upd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHYMASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N'LINKED (GLONAC. .) (POTENTIAL).
N'LINKED (GLONAC. .)
1: U38521; AAA91160.1; -.

Li U38463; AAA91159.1; -.

SP; P23946; IKLT.

LEROPS; SO1.140; -.

InterPro; IPRO01254; Peptidase S1.

InterPro; IPRO01254; Peptidase S1.

InterPro; IPRO01254; Peptidase S1.

InterPro; IPRO01314; Peptidase S1A.

Emi; PRO0032; LTYPSin; 1.

PROSITE; PRO0032; LTYPSin; 1.

PROSITE; PRO0134; TRYPSIN DOM; 1.

PROSITE; PRO0135; TRYPSIN DOM; 1.

"QCITE; PSO0135; TRYPSIN HIS; 1.

"QCITEROR RELAY SYSTEM (BY S1) CHARGE STAN CH
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LLPLPLLLL 11
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7; Conserve
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PIR; A39873; JQ0708.
HSSP; P20693; JHLJ.
Interpro; IPR001094; Lectin_C.
Fram; PP00059; lectin_C; 1.
SWART; SM0034; CLECT; 1.
PROSITE: PS00415; C_TYPE_LECTIN_I; 1.
PROSITE: PS0041; C_TYPE_LECTIN_Z; 1.
Glycoprotein; Lectin; Signal; Calcium.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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		RESULT 1  OBNENG  AC OBNENG  D 01-OCT-2002 (TrEMBLrel. 22, Created)  DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence upd  OC SUKATYOLA: Metazoa; Chuman)  OC Bukaryota; Metazoa; Chriman; Stratum corneum).  OC Mammalia; Eucheria; Primates; Cararhini; Hom  OX NCBL TaxID=806;  RS SEQUENCE FROM N.A.  RP SEQUENCE FROM N.A.  RC Strausberg R.;  RA Strausberg R.;  RA Strausberg R.;  RC STRSUB-Skin;  RC SCO0004263; F:Chymotrypein activity; IEA.  DR GO; GO:0004285; F:Peptidase Si.  DR GO; GO:0004285; F:Peptidase Si.  DR GO; GO:0004285; F:Peptidase Si.  DR FRINTS: PRO0124; Peptidase Si.  DR FRINTS: PRO0124; Peptidase Si.  DR FRANT: PRO0134; Peptidase Si.  DR FRANT: PRO0134; Peptidase Si.  DR ROSITE; PSO0134; TRYPSIN, U.  DR ROSITE; PSO0134; TRYPSIN, DR  KW Hydrolase; Protease; Serine procease.  SEQUENCE 253 AA; 27608 MN; 206886A41B22A6  CUELY MATCh

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01-MAR-2002 (TrEMBLrel, 20, Last sequence update)
01-MAR-2002 (TrEMBLrel, 20, Last sequence update)
Similar to RIKEN cDNA 1110002023 gene.
MNS musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Salivary gland;
Strauberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021345; AAH21345.1;
SEQUENCE 73 AA; 7819 MW; 93B8F53399BF3C11 CRC64;
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC0225900; ARH22900.1; -...
MGD; MGI:1913370; Fkbp11...
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InterPro; IPR001179; FKBP_PPIase.
Pfam; PF00254; FKBP; 1.
PROSITE; PS0043; FKBP PPIASE 1; 1.
PROSITE; PS50059; FKBP PPIASE 1; 1.
SEQUENCE 104 Aa; 11085 MW; 0534D57467566914 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to RIKEN CDNA 1110002023 gene.
FKBP11 0R 1110002023RIK.
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STRAIN=Taiwan,
MEDLINE=21844071; PubMed=11853398;
Con L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
Lo C.F., Kou G.H.;
"Identification of a nucleocapsid protein (VP35) gene of shrimp white
spot syndrome virus and characterization of the motif important for
targeting VP35 to the nuclei of transfected insect cells.";
Virology 293:44-53(2002).
                                                                                                                                                                                                                                                                                                                                                                      syndrome
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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MEDINE=20517548; PubMed=11062040;
MEDINE=20517548; PubMed=11062040;
MEDINE=20517548; PubMed=11062040;
MEDINE=20517548; PubMed=11062040;
MEDINE=205175100 C.J.,
MEDINE=205175100-110(2000).
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                                                                                                                      SEQUENCE FROM N.A. PubMed=11689662; MEDINE=2154811; VARIOR F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.; "Complete genome sequence of the shrimp white spot bacilliform
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STRAIN-1-
Lo C.-F., Kou G.-H.,;
Lo C.-F., Kou G.-H.,;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP332093, AAL33136.1;
EMBL, AP440570; ALB9055.1;
EMBL, AP440570; ALB9055.1;
TOWN'S 800910C7FFA0EC7E CRC64;
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cation transport P-type ATPase.
01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Wsv132 (WSSV187).
                                                          White spot syndrome virus (WSSV).
Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
NGBI_TaxID=92652;
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MEDLINE=21359325; PubMed=11466286;
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J. Virol. 75:11811-11820(2001).
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Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; Molf Y.I., "Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

"Genome sequence and comparative analysis of the solvent-producing J. Bacterium Clostridium acetobutylicum.";

"Genome sequence and comparative analysis of the solvent-producing Datterium Clostridium acetobutylicum.";

"BMBL; AE007714; AAK80095.1; -.

"EMBL; AE007714; AAK80095.1; -.

"GO; GO:0016622; F.ATP binding; IEA.

"GO; GO:0016622; F.ATP binding; IEA.

"GO; GO:0016622; F.ATP binding; IEA.

"GO; GO:0016787; F.Hydrolase activity; IEA.

"GO; GO:0016787; F.Hydrolase activity; IEA.

"GO; GO:0016787; F.Hydrolase activity; IEA.

"GO; GO:0016787; F.Hydrolase EI-E2.

"GO; GO:0016787; F.Hydrolase."

"A GO; GO:0016787; F.Hydrolase."

"InterPro: IPR00157; ATPase."

"InterPro: IPR00589; H.Hydrolase."

"InterPro: IPR00689; H.Hydrolase."

"InterPro: IPR00689; H.Hydrolase."

"InterPro: IPR00122; EI-E2_ATPase."

"A Ffam; PF00689; Cation ATPase."

"B Ffam; PF00689; Cation ATPase."
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"Byolution of the Integral Membrane Desaturase Gene Family in Moths
"Byolution of the Integral Membrane Desaturase Gene Family in Moths
and Files.";

"Bunitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF842910; AAW28485.1;

EMBL, AF842910; AAW28485.1;

R GO; GO:0005020; C:membrane; IEA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016020; F:iron ion binding; IEA.

R GO; GO:0016468; F:stearoyl-CoA 9-desaturase activity; IEA.

R GO; GO:000633; P:fatty acid biosynthesis; IEA.

R InterPro; IPRO1522; Desaturase.

R InterPro; IPRO1524; FA desaturase.

R Pfam; FF00487; FA desaturase.

R Pfam; FF00487; FA desaturase.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Acyl-CoA desaturase (Fragment).
Helicoverpa assulta (Oriental tobacco budworm).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera, Endopterygota, Lepidoptera, Glossata; Ditrygia; Noctuoidea;
Noctuidae; Helicothinae; Helicoverpa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               845 AA; 93779 MW; 401293AA1FF9D757 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PROOLIS; CATATPASE.
PRINTS; PROOLISC, HATPASE.
TIGREAMS; TIGRO1494; ATPASE.
PROSITE; PSOOLIS4; ATPASE_E1_E2; 1.
COMPLEE PICTEONE.
SEQUENCE 845 A4, 93779 WW; 401293A1
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PRINTS; PR00075; FACDDSATRASE.
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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28MZZO

10 CORMZZ

11 CORMZZ

12 CORMZZ

13 CORMZZ

14 CORMZZ

15 CORMZZ

16 CORMZZ

16 CORMZZ

17 CORMZZ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=98152303; PubMed=9491603;
Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;
"Molecular systematics and paleobiogeography of the South American
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Arvicolinae,
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NADH dehydrogenase subunit 4 (EC 1.6.5.3) (NADH-ubiquinone
oxidoreductase chain 4) (Pragment).
                                                                                                                 Query Match 87.5%; Score 35; DB 5; Length 183; Best Local Similarity 87.5%; Pred. No. 33; Matches 7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 87.5%; Score 35; DB 8; Length 208; Best Local Similarity 77.8%; Pred. No. 37; Matches 7; Conservative 2; Mismatches 0; Indels
                                                  183 AA; 21196 MW; 728DA94FAFCD14FA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clethrionomys gapperi (Southern red-backed vole).
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Pfam; PF01059; oxidored q5 N; 1.
PRINTS; PR01437; NUOXDRDTASE4.
NAD; Oxidoreductase; Ubiquinone; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                              PRT;
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ProDom, PD002221, Desaturase; 1. NON TER 1 183 NON TER 183 SEQUENCE 183 AA; 21196 MW; 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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99 LVPLQILLI 107
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                                                                                                                                                                                                                2 LPLQILL 9
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Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

MEDLINE-20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holf R.A., Evens C.A., Gocayne J.D.,

Adamanatides P. G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Burndon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B.D.,

Nun K.H., Doyle C., Baxter E.G., Helf G., Nelson C.R., Gabor G.L.,

Abril J.F., Agdayani A., An H.J., Andrews-Pénnkoch C. Baldwin D.,

Ballew R.M., Bence P.V., Berman B.P., Bandari D., Bolhakov S.,

Berson K.Y., Bence P.V., Berman B.P., Bandari D., Bolhakov S.,

Borkova D., Botchan M.R., Bouck J., Broketein P., Eccher M., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenpoort L.B., Davies P.,

Burtis K.C., Evangelista C.C., Ferraz C., Cerrera S., Plaischman W.,

Geloden K., Doup L.B., Downes M., Digat. Rocha S., Durkov B.C., Dunn P.,

Durbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Cerrera S., Plaischman W.,

Foels C., Gobbiellan A.E., Gary N.S., Gelbart W.M., Glasser K.,

Glodek A., Gong F., Gorrell J.H., Gu Z., Galbart W.M., Glasser K.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Harris N.L., Marvey D., Heiman T.J., Mernison J.A., Ketnikon J.A.,

Alalai M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketnikon J.A.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,

Alazzolo M., Pittman G.S., Pan S., Pollard J., Puri W., Relson D.L.,

Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri W., Relson D.L.,

Albazzolo M., Pittman G.S., Pan S., Pollard J., Puri W., Smith T.,

Spier E., Spradiing A.C., Stapleton M., Stupski M.P., Smith T.,

Spier E., Spradiing A.C., Stapleton M., Stupski M.P., Smith H.O.,

Alban Wang Z.Y., Wassarman D.A., Weinsenbach J.,

Alban W. H. F., Zavori J.S., Zhon Y., Wein S.,

Gience Sequence of Drosophila melangaste
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Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,

Banzon J., Adams J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A carlson J.W., Entie E., Calle R.F., Garg N.S., George R.A.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalal, W. Kruse D., Li P., Mattei B., Moshrefi A.,

McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

B pacleb J., Paragas V., Park S., Parel S., Petelffer B.,

Phousnenavong S., Pittman G.S., Paris N., Patchards S., Scheler F.,

Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Williams S.M., Zaverij J.S., Smith H.O., Vener J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Thuy J.L., Bergman C., Berman B., Carlson J. M., Celniker S.E., Clampy J.L., Bergman C., Berman B., Carlson J. M., Cey A., Harris N., Kromiller B., Marshall B., Milburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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MEDLINE-99120557; PubMed=9921682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Gold B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria, Proteobacteria, Bpsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
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GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0015385; F:scadium.inydrogen antiporter activity; IEA.

GO; GO:0006885; F:regulation of pH; IEA.

InterPro: IPR04770; Antiport_nhaC.

Pfam; PF03553; Na H_antiporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.5%; Score 35; DB 16; Length 493;
88.9%; Pred. No. 83;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                      Query Match 87.5%; Score 35; DB 5; Length 233; Best Local Similarity 77.8%; Pred. No. 41; Matches 7; Conservative 2; Mismatches 0; Indels
                                                                             FlyBase; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                           EMBL; AE003782; AAN11138.1; -.
FlyBase, FBGH0051600; CG31600.
InterPro; IPR000301; Transmem 4.
SEQUENCE 233 AA; 26529 MW; 4A6086B9238EB329 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          493 AA; 53597 MW; 7F19A079A844A962 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last Sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Conserved hypothetical integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                       493 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999)
EMBL, AE001518; AAD06464.1; -
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                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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77 LIPLQILVL 85
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                                                                                                                                                                                                                                                           1 LLPLOILLL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative.
JHP0880.
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AC 025600
DT 01-JAN
DT 01-JAN
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Q9ZKQ5
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182 182
182 AA; 21228 MW; 056448B6D0CC4121 CRC64;
NON TER
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Matches
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A Knipple D.C., Rosenfield C.L., You K.M., Jeong S.E.;
A Knipple D.C., Rosenfield C.L., You K.M., Jeong S.E.;
and Flies.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
B. Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
B. Rosenfield Flamman F. E.A.
B. GO, GO:0005783; C:endoplasmic reticulum; IEA.
GO; GO:0005783; C:endoplasmic reticulum; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016526; F:iron ion binding; IEA.
GO; GO:0016521; P:farty acid biosynthesis; IEA.
R. GO; GO:0016522; Decaturase.
R. InterPro; IPROS804; FA_desat_fam.
R. FINTER: PRO08687; FA_desaturase:
R. PRINTS; PRO08075; FA_CESAT_fam.
R. PRINTS; PRO075; FACDSATRASE.
                                                                                                                 STRAIN=26695 / ATCC 700392;
STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=9252185;
Tomb J.-F., White D., Kerchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Relschmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson M., Khalak H.G., Glodek A., Kchney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Gotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Watter J.C.;
Wenter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia, Noctuoidea, Noctuidae, Hadeninae, Mamestra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                    Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of the gastric pathogen Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:00161385; P:sedlum:hydrogen antiporter activity; IEA.
GO; GO:0006885; P:regulation of pH; IEA.
GO; GO:0006814; P:sedlum ion transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR004770, Antiport_nhaC.
Pfam, PP03553, Na H antiporter; 1.
Hypothetical protein; Complete protecme.
SEQUENCE 496 AA, 53928 MW, 3BAASDDBF14F094B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Acyl-CoA desaturase (Fragment)
Mamestra brassicae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 182 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                            pylori.";
Nature 388:539-547(1997).
BMBL, AE000604; AAD07993.1; -.
PIR; B64638; B64638.
TIGR; HP0946; -
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Matches 8; Conservative
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                                                                                  NCBI_TaxID=210;
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    HP0946.
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01-CCT-2002 (TrEMBLrel. 22, Created)
01-CCT-2002 (TrEMBLrel. 22, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
04-CCT-2003 (TrEMBLrel. 25, Last annotation update)
04-CCA desaurase (Fragment).
05-CCT-2004 interpunctella (Indianmeal moth).
05-CCT-2005 Endopteras, Arthropoda, Hexapoda, Insecta, Pterygota,
05-CCT-2005 Physitinae, Physitinae
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera; Endopterygota, Lepidoptera; Glossata, Ditrysia, Noctuoidea,
Noctuidae, Amphipyrinae; Spodoptera.
NCBI_TaxID=69820;
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Minpple D.C., Rosenfield C.L., You K.M., Jeong S.E.;
"Evolution of the Integral Membrane Desaturase Gene Family in Moths
and Flies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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Match S5.0%; Score 34; DB 5; Length 182; Local Similarity 87.5%; Pred. No. 52; conservative 1; Mismatches 0; Indels
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GO; GO:0005783; C:endoplasmic reticulum; IEA.
GO; GO:0005509; F:iron ion binding; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016481; F:stearoyl-CoA 9-desaturase activity; IEA.
GO; GO:004768; F:stearoyl-CoA 9-desaturase activity; IEA.
GO; GO:006439; P:fatty acid biosynthesis; IEA.
InterPro; IPR001522; Desaturase.
InterPro; IPR00184; FA.desaturase.
FEAM: PF00487; FA.desaturase.
PFINITS; PR0075; FA.CDSATRASE.
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Les 7; Conservative
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14 LPLQILLM 21

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A Knipple D.C., Rosenfield C.L., You K.M., Jeong S.B.;
Thipple D.C., Rosenfield C.L., You K.M., Jeong S.B.;
Thipple D.C., Rosenfield C.L., You K.M., Jeong S.B.;
The and Flies.,
The submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

I. Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

R. Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

R. Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

R. GO; GO:0005783; C:membrane; IEA.

R. GO; GO:0005783; C:membrane; IEA.

R. GO; GO:0004768; F:storn ion binding; IEA.

R. GO; GO:0004768; F:storn ion binding; IEA.

R. GO; GO:0004643; F:stearcyl-CoA 9-desaturase activity; IEA.

R. GO; GO:0004633; F:stearcyl-CoA 9-desaturase activity; IEA.

R. InterPro; IRRO05504; FA desat fam.

R. InterPro; IRRO05504; FA desat fam.

R. PIAM; PRO0457; FA desaturase;

R. RINTS; PRO0075; FACDDSATRASE.

R. RINTS; PRO0075; FACDDSATRASE.

R. RINTS; PRO0075; FACDDSATRASE.

R. RINTS; PRO0075; FACDDSATRASE.

R. RINTS; PRO0075; FACDDSATRASE.
                                             SINCALMENDAY;
Knipple D.C., Rosenfield C.L., You K.M., Jeong S.E.;
"Evolution of the Integral Membrane Desaturase Gene Family in Moths
and Files.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF482944; AAM28519.1;
GO, GO,0005783; C:endoplasmic reticulum; IEA.
GO, GO:0005783; C:endoplasmic reticulum; IEA.
GO, GO:0005783; C:endoplasmic reticulum; IEA.
GO, GO:000506; F:ixcon ion binding; IEA.
GO, GO:000506; F:ixcon ion binding; IEA.
GO, GO:0004789; F:steraroyl-CoA 9-desaturase activity; IEA.
GO, GO:0004789; F:steraroyl-CoA 9-desaturase activity; IEA.
GO, GO:0004789; F:atty acid biosynthesis; IEA.
InterPro; IPRO01522; Desaturase.
InterPro; IPRO0487; FA desaturase.
InterPro; IPRO0221; Desaturase; 1.
RON_TER 182 182
SEQUENCE 182 AA; 21193 MW; GE304DED17BD521B CRC64;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea; Tortricidae; Olethreutinae; Cydia.
NCBI_TaxID=82600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87.5%; Pred. No. 52;
Matches 7; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.0%; Score 34; DB 5; Length 182;
87.5%; Pred. No. 52;
tive 1; Mismatches 0; Indels
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182 AA; 20985 MW; CFD238A73678B47A CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 87.5
Matches 7; Conservative
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SEQUENCE FROM N.A. STRAIN=LPSQ;
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SEQUENCE
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Gaps

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2 LPLQILLL 9

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Gaps
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STRAIN-ATCC 5149 / 3B1;
SURDING-22709201; PubMed=12810954;
BEDLINE-22709201; PubMed=12810954;
BEDLINE-22709201; PubMed=12810954;
BEDLINE-22709201; PubMed=12810954;
BEDLINE-22709201; PubMed=12810954;
BEDLINE, Droege M., Fartmann B., Fischer H.-P., GG Z., Hoerster A., Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G., Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
"The complete genome sequence of the carcinogenic bacterium Helicobacter hepaticus."
Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906 (2003).
BENEL, AEQITA46; APA7744.1;
BENEL, AEQITA46; APA7744.1;
SEQUENCE 242 AA; 28014 MW; 5108E98D41244093 CRC64;
                                                                                                        Helicobacter hepaticus.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=32025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         85.0%; Score 34; DB 16; Length 242; 66.7%; Pred. No. 68; 0; Indels cive 3; Mismatches 0; Indels
                                              Last sequence update)
Last annotation update)
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he : 31.3333 secs
                               Created)
PRT;
                         OLOCT-2003 (TrEMBLrel. 25, La 01-0CT-2003 (TrEMBLrel. 25, La Hypothetical protein. HH0877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 6; Conservative
PRELIMINARY;
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The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCB). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for carcinoma and malignant hyperplasia. The SCCB oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing cancer comprises detecting stratum corneum chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; Page 103; 127pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2001; 2001WO-US003977
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                                                                                                    March 1, 2004, 17:16:55 ; Search time 45.5556 Seconds (without alignments) 55.820 Million cell updates/sec
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Abg23378 Novel
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Abb84421 H
Abb84406 A
Aau8240 A
Abb07441 A
Abros8471 A
Adb80484 A
Aab21328 A
Aac12472 A
Aac12472 A
Aac18472 A
Aac18473 A
Aac18573 A
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Ada05736 F
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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ABU07440
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Length 9;

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RESULT 1 AAE08241 ID AAE08241 XX AC AAE AC AAE XX XX DT 01-1 XX	082 NOV NOV Ser Ser Ser O01	241 stand 241; V-2001 ( stratum um corneu r; ovaria ense thes sapiens.	and ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) ( ) (	standard; 01 (firs' atum corn. orneum ch. varian; b therapy; ens.	standard; peptide;  i  001 (first entry)  ratum corneum chymo corneum chymotrypsi corneum chymotrypsi e therapy; malignan ie therapy; malignan iens.	ide; ry) hymc ypsi i lu	en en hy	izyme peptid SCCE; cytos prostate;	e #6 (residues 4- tatic; vaccine; t carcinoma; human;	. 4-12). ;; tumour; ian;	
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PKT) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed carivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abbarrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from NIPO at the printed specification, but was obtained in the contract of the contr
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                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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Pred. No. 1.4e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human diagnostic protein #23369.
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         100.08; Pr
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23-AUG-2000; 2000US-00649167
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                                           Best Local Similarity 100.
Matches 9; Conservative
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N-PSDB; AAS87565.
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3G23378
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Dipippo VA;
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                                                                                                                   immunomodulator; cytostatic; noorropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                           human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
         ADA05736 standard; protein; 198 AA
                                                                                   Human NOV18c protein SEQ ID NO:96.
                                                                                                                                                                                                                                                                                                                200105-0327435P.
200105-0327449P.
200105-0328029P.
200105-0328044P.
200105-0328046P.
200105-0328056P.
200105-0328046P.
200105-0328056P.
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24-OCT-2001, 2001US-0343629P.
29-OCT-2001, 2001US-0349575P.
01-NOV-2001, 2001US-0346357P.
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2002US-0373815P.
2002US-0373817P.
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28-MAY-2002; 2002US-0383656P.
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2002US-0391335P.
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2002US-0373884P.
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2002US-0381038P
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                                                            (first entry)
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N-PSDB; ADA05735.
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09-OCT-2001; 2
09-OCT-2001; 2
12-OCT-2001; 2
15-OCT-2001; 2
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22-OCT-2001;
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ADA0573
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Query Match
100.0%; Score 40; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 9; Conservative 0; Mismatches 0; Indels

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; Page 170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described and carrier; (2) a kit composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (6) a cell polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a descase associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for a berrant physiclogical interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide, (12) a method for modulation or preventing a pathology associated with the above polypeptide in a method for producing the activity of the polypeptide described above; (13) methods of preacting or preventing a pathology associated with the above polypeptide is useful in manufacturing a medicament for reaging a manufalabetic, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for reaging a pathology associated with the above polypeptide or the nucleic acid molecule may be used to disgnose, treat or prevent metabolic acid molecule may be used to disgnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cancer, and polypeptide associated with a human disease. The polypeptide or paractive present invention.

Sequence 198 AA;

0; Gaps 100.0%; Score 40; DB 6; Length 198; 100.0%; Pred. No. 8.6; 0; Indels iive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.u Bertacal 9; Conservative 

· 4 SLLIPLOIL 12 1 SLLLPLQIL 9

ADA05732 standard; protein; 250 AA. ESULT 4 DA05732 

06-NOV-2003 (first entry) ADA05732;

Human NOV18a protein SEQ ID NO:92.

human; NOVX, antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alaheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.

Homo sapiens

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02-OCT-2002; 2002WO-US031373.
                                                                    2001US-0349575P.
2001US-0346357P.
                                                                              2002US-0373815P.
2002US-0373817P.
2002US-0373826P.
                               2001US-0327917P
                                                                                         2002US-0373884P.
                                                                                                                        01-OCT-2002; 2002US-00262511
                                     09-0CT-2001;
09-0CT-2001;
12-0CT-2001;
15-0CT-2001;
17-0CT-2001;
18-0CT-2001;
22-0CT-2001;
                                                                    29-OCT-2001;
01-NOV-2001;
                                                                           17-APR-2002;
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      10-APR-2003
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(CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerbinsen BD, Anderson DW, Zhong M, Catterton E;
Oit T, W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg MB, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36. N-PSDB; ADA05731.

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New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; Page 169-170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOVI). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the mucleic acid molecule described above; (5) a cell comprising the above vector; (6) an artibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) method for identifying an agent that binds to the polypeptide described a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described to above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to

Sequence 253 AA;

field.)

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a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. NoVX sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obestly, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoletic disorders and various dyslipidaemias. The nucleic cands can also be used as hybridiation probes, in chromosome mapping, tissue typing, preventive medicine and proper incorrer.
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Sequence 250 AA;

Gaps ; 0 100.0%; Score 40; DB 6; Length 250; 100.0%; Pred. No. 11; 0; Indels 0; Mismatches Query Match
Best Local Similarity 100.
Matches 9; Conservative

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AAR67888 standard; protein; 253 AA. ESULT 5

AAR67888;

(revised)
(first entry) 25-MAR-2003 09-AUG-1995

Human stratum corneum chymotrophic recombinant enzyme (SCCE).

Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis; callosities; keratosis pilaris; ichthyoses; eczema.

Homo sapiens

WO9500651-A1 05-JAN-1995. 94WO-IB000166 20-JUN-1994; 93DK-00000725 18-JUN-1993;

(SYMB-) SYMBICOM AB.

Egelrud T, Hansson L;

WPI; 1995-052088/07. N-PSDB; AAQ81203.

Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of specific inhibitors

Disclosure, Page 97; 137pp; English.

The enzyme encoded by this sequence is used in pharmaceutical, cosmetic and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkeratetic conditions (e.g. callosities or keratosis pilaris), ichthyoses, psoriasis, eczema, etc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid p5507. (Updated on 25-MAR-2003 to correct PN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid preptide. Its anino acid sequence was deduced from a cDNA clone (AAT39783) obtd. from a buman lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. E. coli) or eukaryotic and testing of cpds. useful for treating or develop products for the design associated with beta-amyloid peptide, esp. Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human amyloid precursor protein protease - used to develop prods. for the treatment or diagnosis of associated conditions, esp. Alzheimer's disease.
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         Score 40; DB
Pred. No. 11;
                                 0; Mismatches
                                                                                                                                                                                                                          Human amyloid precursor protein protease.
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ID ABB84421 standard, peptide; 253 AA.
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                                                                                                                                                 AAW05383 standard; protein; 253 AA.
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         100.0%;
ilarity 100.0%;
Conservative 0
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N-PSDB; AAT39783.
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                                                                                                                                                                                                                                                                                       Homo sapiens
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(first entry)

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Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
                                                                                                                      SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
                                                       Human SCCE protein N-terminal fragment SEQ ID 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Page 37; 74pp; English
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09-FEB-2001; 2001DK-00000218.
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(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                  WO200262135-A2.
                                                                                                                                                                                                                                                                                                           Homo sapiens.
08-NOV-2002
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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide emparate a significant part of a nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous scce or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a disgnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal phyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation, bruit begidermal hyperkeratosis. The mammal of the invention skin diseases with human stratum corneum chymotryptic enzyme, SCCE transgenic mammals described in the invention
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9; Conservative
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Gaps
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100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 11; ive 0; Mismatches 0; Indels
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SLLLPLOIL 12

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RESULT 8 ABB84406

ABB84406 standard; protein; 253 AA 

ABB84406;

(first entry) 08-NOV-2002

Human SCCE protein.

SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.

Homo sapiens

WO200262135-A2.

15-AUG-2002.

08-FEB-2002; 2002WO-IB001300

09-FEB-2001; 2001CA-02332655. 09-FEB-2001; 2001DK-0000218.

(EGEL/) EGELRUD T. (HANS/) HANSSON L.

ä T, Hansson Sgelrud

WPI: 2002-643380/69. N-PSDB; ABQ76226 Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.

Claim 10; Page 58-59; 74pp; English.

This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence of coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant; operably linked to a promoter that drives expression of heterologous sccor its variant in skin. The product of the invention is useful as a model or ameliorate a pathogenic condition, for development, to relieve or ameliorate a pathogenic condition, for development or testing of a composition affective for the prevention or treatment of an exportant or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an exportant or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an exportant or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an exportance at a topic dermatitis, eczema, acne and inherited skin diseases with epidermal hyperkeratosis. Phe mammal of the invention is also useful or sa model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the human stratum corneum chymotryptic enzyme, SCCE which is a serine protease synonymous with human kallikrein 7 (KLK7) and is used in the development of the

Sequence 253 AA;

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.. 0 100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 11; tive 0; Mismatches 0; Indels 9; Conservative Query Match Best Local Similarity Matches

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SLLLPLOIL 12 1 STLLPLQIL 9

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Amino acid sequence of novel human protease #39
AAU82740 standard; protein; 253 AA
                                                                                      (first entry)
                                                                                         23-APR-2002
                                            AAU82740;
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Human, protease, cancer, immune-related disorder, cardiovascular disease, neuronal-associated disease, metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme 26-JUN-2000; 2000US-0214047P. 26-JUN-2001; 2001WO-US020171. (SUGE-) SUGEN INC WO200200860-A2 Homo sapiens. 03-JAN-2002.

Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory Caenepeel Sudarsanam S, Manning G, Whyte D, WPI; 2002-139913/18. N-PSDB; ABK31782. Plowman G, W

Claim 6; Fig 2N; 313pp; English.

The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, cloun, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asbhma), cardiovascular diseases (e.g. inflammatory diseases and asbhma), brain or neuronal-associated diseases, metabolic coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. disorders) conformatorial aspociated disorders, confiction sexual dysfunction, mood disorders, attention disorders, neurological disorders (e.g. Alzhehmer's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel human proteases of the invention

Sequence 253 AA;

Gaps 0 100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 11; 0; Mismatches 0; Indels Query Match
Best Local Similarity 100...
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RESULT 10 ABU07440

ABU07440 standard; protein; 253 AA

ABU07440;

(first entry) 28-JAN-2003 Protein differentially regulated in prostate cancer #43.

Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring.

Homo sapiens.

WO200281638-A2. 

17-0CT-2002.

08-APR-2002; 2002WO-US010824.

06-APR-2001; 2001US-0281731P. 06-APR-2001; 2001US-0281732P.

(ORIG-) ORIGENE TECHNOLOGIES INC.

Jay G; Sun Z, WPI; 2003-058520/05. N-PSDB; ABX10343.

Novel genes which are differentially regulated in prostate cancer, used for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

Claim 1; Page 293-294; 416pp; English.

prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves certaining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Preferably, the expression levels of at least 10 genes are determined.

(I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells which involves contacting a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of a prostate cancer cells with a test agent under conditions effective for is useful as molecular markers, as drug targers, and for detecting, preventing or treating, determining predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of conditions especially relating to prostate cancer. (I) and its stage of development, the nature of genetic defect, etc. The polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus considering apprications to treat prostate cancer. The identification of prostate cancer. The identification of searching to prostate cancer. The identification of the polypeptide of genes, and groups of genes, any argumes of genes, and groups of genes. of specific genes, and groups of genes, expressed in pathways physiologically relevant to prostate cancer permits the definition of functional and disease pathways and the delineation of targets in these pathways which are useful in disquostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein diferentially applications. This is the am regulated in prostate cancer

Sequence 253 AA;

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The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves intervention in a subject having a prostate cancer, which involves carget genes which are differentially-regulated in prostate cancer. Freferably, the expression levels in a sample comprising prostate tissue of tracet genes which are differentially-regulated in prostate cancer. Freferably, the expression levels of at least 10 genes are determined. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated activity of activity of a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful for sasessing, monitoring, prognosticating, preventing, attaing, assessing, monitoring, prognostication, of diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer e.g., in tissue sections, in biopsy sample, in total RNA, in lymph, in blood cate. (I) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. The polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
                                                 Gaps
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ilarity 100.0%; Score 40; DB 6; Length 253; 100.0%; Pred. No. 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Protein differentially regulated in prostate cancer #74.
                                                                                                                                                                                                                                                               ABU07471 standard; protein; 253 AA.
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for searching specific binding partners of the polypeptide. (I) is useful in therapeutic applications to treat prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways physiologically relevant to prostate cancer permits the definition of functional and disease pathways and the delineation of targets in these applications. This is the amino acid sequence of a protein differentially regulated in prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide and polypeptide useful for diagnosing and/or treating cancer, particularly ovarian cancer, and as a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
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Best Local Similarity
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                                                                                                                                                           Sequence 253 AA;
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RESULT 13

)B80484

27-DEC-2002

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The present sequence is human stratum corneum chymotryptic enzyne (HSCEE), a member of the kallikrein multi-gene family. Kallikreins and Kallikrein-like protease enzyme kallikrein-like protease enzyme family. They catalyse the selective cleavage of specific polypeptide precursors to release peptides with potent biological activity. Nucleic acids encoding Kallikrein-like proteins KKLII, KLK-LZ, KLK-LI, KLK-LY, KKK-LS, and KLK-LG have been isolated. The proteins are useful in the treatment, monitoring and diagnosis of cancers, especially prostrate cancer. They can also be used to identify a substance that can associate with or mediate the biological activity of the proteins. Antibodies can be used to treat conditions mediated by the kallikrein-like proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New kallikrein-like (XLK-L) proteins for diagnosing and treating KLK-L protein mediated disorders, especially cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human stratum corneum chymotrypsin enzyme peptide #3 (residues 5-13).
                                                  Human, KLK-L1, KLK-L2, KLK-L3, KLK-L5, KLK-L5, KLK-L6, HSCEE,
human stratum corneum chymotryptic enzyme, kallikrein-like protein,
serine protease, cytostatic, cancer, prostrate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 40; DB 3; Length 257; 100.0%; Pred. No. 11; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Fig 17; 184pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE08238 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                 99US-0124260P.
99US-0127386P.
99US-0144919P.
                                                                                                                                                                                                                                                                                                                                                                                                         (MOUN ) MOUNT SINAI HOSPITAL
                                                                                                                                                                                                                                                                       39-MAR-2000; 2000WO-CA000258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yousef GM, Diamandis EP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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01-APR-1999;
21-JUL-1999;
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AAE08238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method of detecting an ovarian cancerassociated transcript in a cell from a patient, by contacting a blological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to any of one of 80 nucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer and in identifying and using agents and/or targets that inhibit ovarian cancer. The nucleic acid molecule, polypeptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, and as vaccines. This sequence corresponds to one of the proteins used for the detection method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                  cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection.
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                         ADB80484 standard; protein; 253 AA
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27-AUG-2001, 2001US-0315287P.
05-SEP-2001, 2001US-031544P.
13-NOV-2001; 2001US-035066EP.
12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-2002; 2002WO-US019297
                                                                                                            (first entry)
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Matches 9; Conservative
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N-PSDB; ADB80483.
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Gaps

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16-AUG-2001

(first entry)

02-FEB-2001

AAB21326;

RESULT 14 VAB21326

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07-FEB-2001; 2001WO-US003977.
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11-FEB-2000; 2000US-00502600.

(UYAR-) UNIV ARKANSAS.

O'brien TJ;

WPI; 2001-514676/56.

Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme.

Claim 25; Page 102; 127pp; English.

The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proceases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

Sequence 9 AA;

0; Gaps Query Match 90.0%; Score 36; DB 4; Length 9; Best Local Similarity 100.0%; Pred. No. 1.46+06; Matches 8; Conservative 0; Mismatches 0; Indels

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2 LLLPLQIL 9 |||||||| 1 LLLPLQIL 8

earch completed: March 1, 2004, 17:28:53 ob time : 46.5556 secs

us-09-905-083-36.rai

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ORGANISM: Homo sapiens
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116, App
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                                                                                                                                                               March 1, 2004, 17:21:46; Search time 11.8889 Seconds (Without alignments) 39.081 Million cell updates/sec
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// CGTZ_6/ptodata/2/iaa/PGTUS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-210-084-3
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US-09-489-019A-10791
US-09-489-017323
US-08-676-279-57
US-08-777-715-7
US-08-95-4-18-2
US-08-95-4-18-2
US-08-977-378-22
US-08-977-378-22
US-08-977-378-22
US-08-977-378-22
US-08-977-378-22
US-08-378-24
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US-08-378-28
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US-08-378-28
US-08-378-28
US-08-378-28
US-08-378-28
US-08-378-28
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## ALIGNMENTS

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Sequence 35, Application US/09502600A

Sequence 36, Application US/09502600A

Patent No. 6294344

GENERAL INVENTION:
TITLE OF INVENTION:
Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION:
OURSENT PILING DATE: 2000-02-11
CORRENT FILING DATE: 2000-02-11
CORRENT FAPLICATION NUMBER: US/09/502,600A

PRIOR PILING DATE: 03-14-1998

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 36

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: O'Exien, Timothy J.

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
FILE REFERENCE: D6223CIP(C/D/CIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT FILING DATE: 2001-07-13

PRIOR PILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 36

LENGTH: 9

LENGTH: 9

TYPE: PRT

CREANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Residues 4-12 of the SCCE protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 40; DB 3;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 9; Conservative 0; Mismatches 0
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; Patent No. 6627403
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Gaps
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Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Egglrud, Torbjorn
APPLICANT: Bgelrud, Torbjorn
APPLICANT: Baseon, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF SEQUENCES:
NUMBER OF SEQUENCES:
ADDRESSE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IB PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUPERATURS SISTEM: FC-LOS/MS-COS
SOFTWARE: PARENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REJECTANTON NUMBER: 13,372
REJECTANTON NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 antho acids
TTPE: Antho acids
TTPE: Antho acids
                                                                                                         100.0%; Score 40; DB 4; Length 9; 100.0%; Pred. No. 3e+05; ative 0; Mismatches 0; Indels
FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 4-12 of the SCCE protein
-09-918-243-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08824874
Patent No. 5652300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
                                                                                    Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 SLLLPLOIL 12
                                                                                                                                                                                                1 SLLLPLQIL 9
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JS-08-824-874-3
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US-09-154-344-2
) Sequence 2, Application US/09154344
) Sequence 2, Application US/09154344
) Patent NO. 5981256
GENERAL INFORMATION:
APPLICANT: Hagalrud, Torbjorn
APPLICANT: Hansson, Lennart
ITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
ITLE OF INVENTION: Bnzyme (SCCE)
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 100.0%; Score 40; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DCS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
                                                                                                                                                 COMPUTER: Diskette
COMPUTER: IBM COMPALISE
SOFTWARE: SASTEM: DOS
SOFTWARE: FASTEGG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFCATION: 514
PRIOR APPLICATION NUMBER:
FILING APPLICATION DATA:
FILING APPLICATION NUMBER:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF-0252 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LIBRARY: GenBank
; CLONE: 532504
US-08-824-874-3
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                                                                        Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 10036-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                           USA
                                                                                                                                              94304
                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
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us-09-905-083-36.rai

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Gaps

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            Query Match 100.0%; Score 40; DB 3; Length 253; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Score 40; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                         RESULT.

US-09-210-084-3

Sequence 3, Application US/09210084

Sequence 3, Application US/09210084

Revent No. 6197811

GENERAL INFORMATION:

APPLICANT: Hillman Jennifer L.

APPLICANT: Hillman Jennifer L.

APPLICANT: Lal, Preeti

TITLE OF INVENTION: NOVEL KALLIKREIN

ITLE OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSER: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/09/210,084
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECHONICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09764762
; Patent No. 6472195
; GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
ITTLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHERACTERISTICS: LENGTH: 253 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                 4 SLLLPLOIL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SLLLPLQIL 9
                                                                                                       1 SILLPLOIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 532504
US-09-210-084-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dixon, Eric P.
APPLICANT: Dixon, Eric P.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: RELATED NUCLEIC ACIDS
TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bil Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 40; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/OCKET NUMBER: 35,372
REFERENCE/OCKET NUMBER: 1103326-181
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECAX: (212) 819-8783
TELECAX: (212) 819-8783
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 253 amilio acids
TYPE: amilio acid
TYPE: amilio acid
TYPE: amilio acid
TOPOLOGY: linear
MOLECULE TYPE: procein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Indiana COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESULT 6
S-08-930-188-2
Sequence 2, Application US/08930188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLCGY: linear
MOLECULE TYPE: protein
JS-08-930-188-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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STRANDEDNESS: si:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                             3-09-154-344-2
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Gaps

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Query Match 90.0
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 SLLLPLOIL 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Shella P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 40; DB 4; Length 253; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION AUNBER: 09/210,084
FILING DATE: AUNKNOWN>
APPLICATION NUMBER: 09/210,084
FILING DATE: AUNKNOWN>
ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCEY DOCKET NUMBER: PF-0252 US
TELEFANE THE - 85-0555
TELEFAX: 415-85-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE TO THIS STATE OF THE STATE OF
                          ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA
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SEQUENCE DESCRIPTION: SEQ ID NO: 3: S-09-764-762-3
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TYPE: amino acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
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IMMEDIATE SOURCE:
LIBRARY: GenBank
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CT-US96-04294-2
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PROPRABLICATION NUMBER 109/416.257

**TILING DATE: 104.262.209416.257

**ATTOWNST INCOMMATION:
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**TEREPORT: 137.277.1090

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Sequence 35. Application US/09918243
; Sequence 35. Application US/09918243
; Patent No. 6627403
; GARERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Satin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
FILE PREPERENCE: D6223GIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT APPLICATION NUMBER: US
CURRENT APPLICATION NUMBER: US
RIOR APPLICATION NUMBER: US
; RIOR PILING DATE: 2001-07-30
; RIOR PILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 35
                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT:
O'STIEN, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Ovarian Cancer
FILE REFERENCE: D6223CIP-C
CURRENT APPLICATION NUMBER: U9/039,211
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR PELING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 16
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-918-243-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ). OTHER INFORMATION: Residues 2-10 of the SCCE protein US-09-502-600-116
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100.0%; Pred. No. 3e+05;
tive 0; Mismatches 0
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100.0%; Pred. No. 3e+05;
iive 0; Mismatches
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                                                                                                                                                      US-09-502-600-116
; Sequence 116, Application US/09502600A
; Patent No. 6294344
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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                                                        1 LLPLOIL
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US-09-918-243-35
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Sequence 12075, Application US/09489039A
Patent No. 6610836
Patent No. 6610836
Patent No. 6610836
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PRIBWONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PRILING DATE: 2000-10.27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PRILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12075
IENGTH: 912
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Parent No. 6294344

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Owner of the Concer-
TITLE OF THE PREFERENCE: D622GIP-C
CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: 03/039/211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 35
ILENGTH: 9
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Pred. No. 94;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                        90.0%; Score 36; DB 4; Length 9; 100.0%; Pred. No. 3e+05; Live 0; Mismatches 0; Indels
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OTHER INFORMATION: Residues 6-14 of the SCCE protein US-09-502-600-35
                                                                                                                                            NAWE/KEY: CHAIN
OTHER INFORMATION: Residues 5-13 of the SCCE protein
IS-09-918-243-33
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ORGANISM: Klebsiella pneumoniae
JS-09-489-039A-12075
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 33
LENGTH: 9
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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ALIGNMENTS
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Patent No. US20020146708A1
GENERAL INFORMATION:
9; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 9; Conserva
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Sequence 38, Appl
Sequence 34, Appl
Sequence 90, Appl
Sequence 498, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 33, Appl
Sequence 13, Appl
Sequence 116, Appl
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                                                                                                             March 1, 2004, 17:35:01; Search time 24.1111 Seconds (without alignments) 78.818 Million cell updates/sec
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1: /cgm2_6/prodated/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgm2_6/prodated/1/pubpaa/PCT_MBW_PUB.pep:*

3: /cgm2_6/prodated/1/pubpaa/US06_NBW_PUB.pep:*

4: /cgm2_6/prodated/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgm2_6/prodated/1/pubpaa/US07_NBW_PUB.pep:*

6: /cgm2_6/prodated/1/pubpaa/US08_NBW_PUB.pep:*

7: /cgm2_6/prodated/1/pubpaa/US08_PUBCOMB.pep:*

8: /cgm2_6/prodated/1/pubpaa/US08_PUBCOMB.pep:*

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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-905-083-36
US-09-905-083-36
US-09-764-762-3
US-09-764-762-3
4 US-10-264-283-90
5 US-10-13-999-48
US-09-918-243-3
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; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-918-243-36
                        US-10-302-267-1488
US-10-302-267-1488
US-10-050-882-131
US-10-050-882-131
US-10-050-882-131
US-10-066-818A-338
US-10-006-818A-338
US-10-006-818A-338
US-10-015-869A-338
US-10-015-869A-338
US-10-012-913A-338
US-10-017-913A-338
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CITY: Palo Alto

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4 SLLLPLQIL 12
                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SLLLPLQIL 9
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Best Local Similarity
Matches 9; Conserv
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APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Barly Diagnosis of
TITLE OF INVENTION: Ovarian Cancer
FITLE OF INVENTION: Ovarian Cancer
FILE REFERENCE: D6223GIP/C/Dia
CURRENT APPLICATION NUMBER: US/09/905,083
PRIOR APPLICATION NUMBER: US 09/502,600
PRIOR PILING DATE: 2000-02-11
SEQ ID NO 36
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 40; DB 9; Length 9; 100.0%; Pred. No. 7.1e+05;
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                                                                                                                                                                                                                                                                                                           NAME/KEY: CHAIN
OTHER INFORMATION: Residues 4-12 of the SCCE protein
S-09-905-083-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hillman, Jennifer L.
Lal, Preeti
TILLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 98, Application US/0988615
Sequence 98, Application US/0988615
Sequence 98, Application US/0988615
Sequence 98, Application US/0988615
Setent No. US2020064856A1
APPLICANT: PLOWMAN, GREGORY
APPLICANT: CARNEDEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: SUDARSANAM, SUCHA
APPLICANT: NOWER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
RADOR APPLICATION NUMBER: 60/214,047
PRIOR PILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFFWARE: PALENT NOS: 150
SOFFWARE: PALENT NOS: 150
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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IS-09-764-762-3
Sequence 3, Application US/09764762
Setence No. US20020068341A1
BELEN NO. US20020068341A1
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
IS-09-888-615-98
                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 90, Application US/10264283
Publication No. US2003014494A1
SEQUENCE INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND DISCORDER OF THE REPERENCE: 210121.590
CURRENT PAPLICATION NUMBER: US/10/264,283
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 111
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 90
LENGTH: 253
TYPE: PRT
CORGANISM: Homo sapiens
US-10-264-283-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 40; DB 14; Length 253; 100.0%; Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: DISKette
COMPUTER: IBM Compatible
CORPOTER: IBM COMPATIBLE
APPLICATION NUMBER: US/09/764,762
FILING DATE: I6-Jan.2001
CLASSIFICATION NUMBER: 09/210,084
FILING DATE: CURKNOWN:
ATTORNEY/AGENT INFORMATION:
NAMME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 253 amino acida
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
INMEDIATE SOURCE:
LIBRARY: GenBank
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Best Local Similarity 100.
Matches 9; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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CRGANISM: Homo sapiens
US-10-173-999-48
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           Sequence 499, Application US/10295027

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT Afar, Daniel

APPLICANT Afar, Daniel

APPLICANT Girmsery, Wandy M.

APPLICANT Girmsery, Wandy M.

APPLICANT: Girmsery, Wandy M.

APPLICANT: Girmsery, Wandy M.

APPLICANT: Girmsery, Richard

APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: Wack, David H.

APPLICANT: Wack David H.

APPLICANTON: Wack David H.

PRIOR APPLICANTON NUMBER: US 60/350,666

PRIOR APPLICANTON NUMBER: US 60/332,464

PRIOR PLING DATE: 2001-11-12

PRIOR APPLICANTON NUMBER: US 60/3340,375

PRIOR APPLICANTON NUMBER: US 60/3340,375

PRIOR APPLICANTON NUMBER: US 60/3347,211

PRIOR APPLICANTON NUMBER: US 60/3347,214

PRIOR APPLICANTON NUMBER: US 60/347,214

PRIOR APPLICANTON NUMBER: US 60/347,214

PRIOR APPLICANTON NUMBER: US 60/347,214

PRIOR APPLICANTON NUMBER: US 60/347,249

PRIOR APPLICANTON NUMBER: US 60/347,249

PRIOR APPLICANTON NUMBER: US 60/355,250

PRI
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Sequence 48, Application US/10173999
Sequence 48, Application US/10173999
Publication No. US20040005563A1
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Gish, Kurt C.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cvarian Cancer, Compositions
TITLE OF INVENTION: Cancer
FILE REFERENCE: 018501-002420US
CURRENT SPPLICATION NUMBER: US/10/173,999
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/299,234
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100.0%; Score 40; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0
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JS-10-295-027-498
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S-10-295-027-498
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; Sequence 33, Application US/09905083
; Ratent No. US20020146708A1
; GENERAL INFORMATION:
    APPLICANT: O'Srien, Timothy J.
    TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
    TITLE OF INVENTION: O'varian Cancer
    TITLE OF INVENTION: O'varian Cancer
    TILE BEBERROE: D6223CIP/C/Div
    CURRENT FILIKO DATE: 2001-07-13
    PRIOR PLIING DATE: 2001-07-13
    NUMBER OF SEQ ID NOS: 136
; NUMBER OF SEQ ID NOS: 136
; LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 33, Application US/09918243

Patent No. US20020142317A1

GENERAL INFORMATION:

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REFERENCE: D6223CIP/C/D/CIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 33

LENGTH: 9
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14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CHAIN
OTHER INFORMATION: Residues 5-13 of the SCCE protein US-09-918-243-33
                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/315,287
PRIOR PILING DATE: 2001-08-27
PRIOR PILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 48
LENGTH: 253
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Best Local Similarity 100.
Matches 9; Conservative
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RESULT 12
US-09-918-243-35
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Sequence 10255, Application US/10369493
Publication No. US20030233675A1
Publication No. US20030233675A1
Publication No. US20030233675A1
APPLICANT: Cao, Yongwei
APPLICANT: Galdman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF WICROBIAL PROPERTIES FILE REFERENCE: 38-10(5262) B
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT APPLICATION NUMBER: US 60/360, 039
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10255
LENGTH: 868
LENGTH: 868
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88.9%; Pred. No. 3.8e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                   90.0%; Score 36; DB 9; Length 9; 100.0%; Pred. No. 7.1e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28, Application US/10236055A
Publication No. US20030134328A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
GOTTON:
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APPLICANT:
FORTSTHE, Methods
APPLICANT:
FORTSTHE METHODS
APPLICANTION:
METHODS
APPLICANTION
METHODS
APPLICANTION
FILING
DATE:
2003-02-28
PRIOR APPLICATION
NUMBER:
US 60/317,988
PRIOR APPLICATION
NUMBER:
SEQ ID NOS:
SEQ ID NOS:
SEQ ID NOS:
LENGTH:
BO4
TYPE: PRT
ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 5-13 of the SCCE protein 5-09-905-083-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Cytophaga hutchinsonii
S-10-369-493-10255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Mus musculus
IS-10-236-055A-28
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                                                                                                                                                                                                                                                                                                                      1 LLLPLOIL 8
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IS-10-236-055A-28
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Sequence 115, Application US/09918243

Parent No. US20020142317A1

GENERAL INFORMATION:

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REFERENCE: D6222CIP/C/D/CIP

CURRENT PILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US

PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-07-3

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 116

LENGTH: 9
                                                                                                                                                                                                                                         Sequence 35, Application US/09918243

Sequence 35, Application US/09918243

Patent No. US20020142317A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Santin, Alessandro

TILLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REFERENCE: D6223CIP/C/D/CIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT PILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 35

LENGTH: 9
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Query Match

82.5%; Score 33; DB 14; Length 804;
Best Local Similarity 75.0%; Pred. No. 8e+02;
Matches 6; Conservative 2; Mismatches 0; Indels
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEX: CHAIN
OTHER INFORMATION: Residues 2-10 of the SCCE protein US-09-918-243-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CHAIN
COTHER INFORMATION: Residues 6-14 of the SCCE protein US-09-918-243-35
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Matches 7; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 7; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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US-09-918-243-116
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Sequence 116, Application US/09905083
Sequence 116, Application US/09905083
Sequence 116, Application Sequence 116, Applications of Sequence 116, Applications and Methods for the Barly Diagnosis of TITLE OF INVENTION: Compositions and Methods for the Barly Diagnosis of TITLE OF INVENTION: COMPACT CALL
CURRENT APPLICATION NUMBER: US/09/905,083
CURRENT FILING DATE: 2001-07-13
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 116
Sequence 35, Application US/09905083
Sequence 35, Application US/09905083
Sequence 35, Application US/09905083
Sequence 35, Application US/09905083
Sequence 35, Application US/09505083
GENERAL INFORMATION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer FILE REPERENCE: D6223CIP/C/Div CURRENT APPLICATION NUMBER: US/09/905,083
CURRENT PILING DATE: 2000-07-13
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 35
LENGTH: 9
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Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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80.0%; Score 32; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels
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NAME/KEY: CHAIN
CHER INCRMATION: Residues 2-10 of the SCCE protein
US-09-905-083-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CHAIN COTHER INFORMATION: Residues 6-14 of the SCCE protein JS-09-905-083-35
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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Search completed: March 1, 2004, 18:08:52 Job time : 25.1111 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model M protein March 1, 2004, 17:21:01 ; Search time 10.2222 Seconds (without alignments) 84.690 Million cell updates/sec no un

US-09-905-083-36 itle:

1 SLLLPLQIL 9 erfect acore: equence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 coring table:

283366 segs, 96191526 residues earched:

283366 otal number of hits satisfying chosen parameters:

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ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* atabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	einase	prot	icin res	robable transcri	L	probable acyltrans	tax-responsive ele	hepatocarcinogenes		probable succinogl	쓾	ExoT protein - Rhi	probable membrane	hypothetical prote	hypothetical prote	₲		ABC transporter, m	ಹ	antibiotic resista	hypothetical prote	SNF1-related prote	probable membrane	hypothetical prote	O-antigen transpor	probable competenc	vy-chai	othetical	interleukin-2 - go
QI	A53968	N	m	T02912	AC2620	7	JC7300	JC4857	B85327	C49349			861692		C84914	T48649	A98157	AH3130	D83934	D69779	10	B90120	m	A90083	A69149	AE0614	A46136	AC2445	S38662
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interleukin-2 prec interleukin-2 prec probable membrane	hypotherical prote probable phosphate NADH2 dehydrogenas hypotherical prote	cell division prot cytochrome aa3 con probable high affi	conglutinin precur	conglutinin - bovi probable transport
S11488 145913 E96979	743766 739622 717092 G69798	F83598 H84314 T43663	HLHUCE E82656 S33603 JN0450	145878 F91173
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000	0000	0000	0000	30
30 31 32	8 8 8 6 8 4 6 7	. w w w.	4 4 4 4 5 4 5 6	4 4 5 4 5

## ALIGNMENTS

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Serior proteinase SCCE precursor - human
NiAlternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 22-Jun-1999
C;Accession: A53968
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J; Biol. Chem: 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MuID:94308255; PMID:8034709
A;Accession: A53968
A;Accession
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Pred. No. 1.5;
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A,Cross-references: GDB:377730
A;Map position: 7435-7435
C,Superfamily: trypsin, trypsin homology
F;30-245/Domain: trypsin homology
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Best Local Similarity 100.0%;
Matches 9; Conservative 0.
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RESULT 2

CyAccession: H75201
Renonymous, Genoscope submitted to the EMBL Data Library, July 1999
A.Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and the EMBL Data Library, July 1999
A.Reference number: A78001
A.Reference number: A78001
A.Reference number: A78001
A.Residues: Preliminary
A.Rotoscule Type: DNA
A.Residues: 1-146 < KAW>
A.Rotoscule Type: DNA
A.Rotoscule Type C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 08-Sep-2000 hypothetical protein PAB0088 - Pyrococcus abyssi (strain Orsay)

A,Gene: PAB0088 C,Superfamily: Pyrococcus abyssi hypothetical protein PAB0088

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1-acyi-sn-glycerol-3-phosphate acyltransferase plsC [imported] - Agrobacterium tumefacier C; Species: Agrobacterium tumefaciens C; Spacession: Ac2620 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. Frage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClells; Karp, P.; Romero, P.; Zhang, S. Science 294, 2117-2233, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Agrobacterium tumefaciens 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: C97402 C; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001 Entry Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; MuID:2160851; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable acyltransferase (AF232919) [imported] - Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: AC2620
A;Status: prellminary
A;Molecule type: DNA
A;Residues: 1-264 «KUR>
A;Residues: 1-264 «KUR>
A;Cross-references: GB;AE008688; PIDN:AAL41377.1; PID:g17738693; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
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A;Map position: circular chromosome
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                                                       Similarity 100.
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19 ILLPLQLL 26
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A;Molecule type: DNA
A;Residues: 1-264 <KUR>
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                                                                                                                                                                                                                                                                                                         aunorubicin resistance transmembrane protein [imported] - Brucella melitensis (strain 1 ; Species: Brucella melitensis
; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
; Date: 01-Feb-3334 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
; Date: 01-Feb-3334 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess roc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
; Title: The genome sequence of the facultative intracellular pathogen Brucella melitens ; Reference number: Ab3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         robable transcription factor MYB41 [similarity] - Arabidopsis thaliana (fragment)
Alternate names: protein T13/3.220
Alternate names: protein T13/3.220
Alternate names: protein T13/3.220
Alternate names: protein T13/3.220
Alternate and Alternate names: protein T3/3.2200
Accession: T02912; T51654
Accession: T02912; T51654
Accession: M.; Poll, T.; Welzenegger, T.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuel ubmitted to the Protein Sequence Database, February 1999
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Jant J. 16, 253-276, 1998
J.Tile: Towards functional characterisation of the members of the R2R3-MYB gene from Ar
,Reference number: Z14349; MUID:9839469; PMID:9839469
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Note: T1318.220
Note: Intro positions not resolved
Superfamily: unassigned myb DNA-binding repeat proteins; myb DNA-binding repeat homold
Keywords: transcription factor
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Molecule type: DNA
;Residues: 1370 <400.
;Cross-references: GB:AE008917; PIDN:AAL51837.1; PID:g17982584; GSPDB:GN00190
;Experimental source: strain 16M
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                                                                   Gaps
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Pred. No. 57;
2; Mismatches 0; Indels
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         DB 2; Length 146;
                                                             0; Indels
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Molecule type: mRNA
Residues: 1-218 <KRA>
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Experimental source: cultivar Columbia
      Score 38; DB 2
Pred. No. 2.2;
1; Mismatches
         95.0%;
88.9%;
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Best Local Similarity 75.0%;
Matches 6; Conservative
Query Match
Best Local Similarity 88.5
Matches 8; Conservative
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293 ILLPLQVL 300
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66 SLLLPLOII 74
                                                                                                                       1 STITETOIT 9
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A;Gene: AT4g28110
A;Map position: 4
C;Superfamily: barley myb-related protein 3; myb DNA-binding repeat homology
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Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0
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C,Superfamily: hypothetical protein b2046
                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             168 SLLLPLO 174
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Species: Rattus norvegicus (Norway rat)
Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 08-Sep-1997
Stishimoto, T.; Kokura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.
Inchem. Biophys. Res. Commun. 224, 746-751, 1996
Title: HTF: A b-zip transcription factor that is closely related to the human XBP/TREE
Reference number: JC4857
Accession: JC4857
Molecule type: mRNA
Residues: 1-267 < KIS>
Comment: This is a basic-leucine zipper type transcription factor involved in hepatoce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       robele transcription factor MYB41 [imported] - Arabidopsis thaliana
| Species: Arabidopsis thaliana (mouse-ear cress)
| Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
| Accession: 185327 | Accession:
    ax-responsive element-binding protein 5 - mouse (Species: Mus musculus (house mouse)
Species: Mus musculus (house mouse)
Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
Massaki, T.; Noguchi, H.; Kobayashi, M.; Yoshida, M.; Takamatsu, K.
Massaki, T.; Noguchi, H.; Kobayashi, M.; Yoshida, M.; Takamatsu, K.
Ma Res. 7, 187-193, 2000
Ma Res. 7, 187-193, 2000
Mark Res. 7, 187-193, 2000
Mark Reference number: JC7300
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;Mocacule type: DNA
;Mocacule: 1.282 <STO>
;Cross_references: GB:NC_001268; NID:g7269665; PIDN:CAB79613.1; GSPDB:GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Gene: treb5
;Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
;Keywords: leucine zipper; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology degwords: leucine zipper; transcription factor 58-98/Domain: fos/jun DNA-binding domain homology <FUD>
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100.0%; Pred. No. 64;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  .Accession: JC7300
.Molecule type: mRNA
.Residues: 1-266 <MAS>
.Cross-references: DDBJ:AB036745
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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probable transport protein, similar to Wax exoT [imported] - Sinorhizobium meliloti (str. C,Species: Sinorhizobium meliloti
C,Species: Sinorhizobium meliloti
C,Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C,Accession: B95976
R,Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan, Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A,Title: The complete sequence of the 1683-kb pSymB megaplasmid from the N2-fixing endom A,Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asstatus: preliminary
Asstatus: preliminary
Asstatus: DNA
Asstatus: Strain Lorg, S.R.; Publer, A.; Abola, F.; Ampe, F.; Barloy-Hubler, P.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
DL: Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
Astatuors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.;
Astatic The composite genome of the legume symbiont Sinorhizobium meliloti.
Astatic annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: C49349
R;Glucksmann, M.A.; Reuber, T.L.; Walker, G.C.
J;Bacteriol. 175, 7045-7055, 1993
B;Glucksmann, M.A.; Reuber, T.L.; Walker, G.C.
J;Bacteriol. 175, 7045-7055, 1993
A;Title: Genes needed for the modification, polymerization, export, and processing of A;Reference number: A49349; MUID:94042870; PMID:8226646
A;Reference number: A49349
A;Reference number: A49349
A;Reference type: DNA
A;Residues: 1-494 cdLD.
A;Residues: 1-494 cdLD.
A;Residues: 1-494 cdLD.
A;Cross-references: GB:L20758; NID:9393240; PIDN:AAA16050.1; PID:9393249
C;Superfamily: hypothetical protein
C;Keywords: transmembrane protein
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Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Mar-2000
Accession: C49349
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80.0%; Score 32; DB 2; Length 282; 100.0%; Pred. No. 68; 0; Indels ive 0; Indels
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80.0%; Score 32; DB 2; Length 494;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels
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122 SLLIPLOL 129

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C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: G65039
F;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
R;Blattner, The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein At2947360 [imported] - Arabidopsis thaliana
(Species: Arabidopsis thaliana (mouse-ear cress)
(Species: Arabidopsis thaliana (mouse-ear cress)
(Species: O.-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
(SAccession: C84914
(S. A. Kaul, X. Kaul, S.)
(S. A. Kaul, S.)
(S. A. Kaul, S.)
(S. A. Kaul, S.)
(S. A. M.)
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(S. A. M.)
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(SACETERION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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A;Residues: 1-196 <BLAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 303;
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hypothetical protein b2612 - Escherichia coli (strain K-12)
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Pred. No. 1.2e+02;
0; Mismatches 2
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Matches 7; Conserv
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Job time : 10.3333 secs
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A/Molecule type: DNA
A/Residues: 1-303 <STO>
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C84914
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Alternate names: hypothetical protein 03329; hypothetical protein YOR3329c
Alternate names: hypothetical protein 03329; hypothetical protein YOR3329c
Alternate names: hypothetical protein 0329; hypothetical protein YOR3329c
Alternate Nar-1996 #sequence_revision 12-Apr-1996 #text_change 19-Apr-2002
Accession: 861692; 867022
Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banrevi, A.; Sander, C.; Valencia ubmitted to the EMBL Data Library, December 1995
Accession: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome Reference number: 861643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Becker, A.; Xleickmann, A.; Kuester, H.; Keller, M.; Arnold, W.; Puehler, A. ubmitted to the EMBL Data Library, April 1993 .;Description: Analysis of the Rhizobium meliloti genes exoU, exoV, exoW, and exol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: DNA
Residues: 1-622 <VOS>
Cross-references: EMBL:275045; NID:91420348; PID:e252028; PID:91420349; MIPS:YOR137c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
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Stasidues: 1.622 - GEEN>
; Grasidues: 1.622 - GEEN>
; Gross-references: EMBL:X94335; NID:g1262139; PID:e217839; PID:g1164980
; Voss, H.; Benes, V.; Rechmann, S.; Teodoru, C.; Schwager, C.; Paces, V.; Ansorge,
multied to the Protein Sequence Database, July 1996
; Reference number: S66965
; Accession: S67022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                             xoT protein - Rhizobium meliloti
;Species: Rhizobium meliloti
;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-May-2000
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80.0%; Score 32; DB 2; Length 582
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels
```

Superfamily: hypothetical protein b2046

|||:|||: |22 SLLIPLQL 129

1 SLLLPLOI 8

>

Cross-references: EMBL: Z22646

Reference number: S40173

Accession: S40176

Accession: S40176; Status: preliminary Molecule type: DNA; Residues: 1-582 <BEC>

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Gaps .; 0

80.0%; Score 32; DB 2; Length 622; 66.7%; Pred. No. 1.5e+02; tive 2; Mismatches 1; Indels

Local Similarity 66.7 tes 6; Conservative

Query Match

| |:|||:| 141 SALIPLQVL 149

Д

ESULT 14 65039

1 SLLLPLQIL 9

Keywords: transmembrane protein :11-27/Domain: transmembrane #status predicted <TMM>

Experimental source: strain S288C Cross-references: SGD:S0005663

Accession: S61693

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5.1.6 Compugen Ltd.	,	time 6 Seconds ut alignments) Million cell updates/sec				141681				d by chance to have a the result being printed, re distribution.		escription	94-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1
GenCore version 5.1.6 (c) 1993 - 2004 Compug	sing sw model	, 1/:1/:25 ; Search (witho 78.105	36	Gapext 0.5	2070155 residues	g chosen parameters:	000	0% 100% 45 summaries		esults predicted to the score of f the total sco	SUMMARIES	a ID	KLK7 HUMAN   FKL1 MOUSE   IHA TRIVU   1947 XANAC   EM11 MOUSE   ICA47 XANAC   EM12 MOUSE   ICA47 XANAC   EM11 MOUSE   ICA1 MOUSE   ICA4 SCHPO   ICA1 MOUSE   ICA4 SCHPO   IC
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Copyright	protein sea		US-09-905-0 40 1 SLLLPLQIL	BLOSUM62 Gapop 10.	141681 8	hits sati	length: ( length: 2	: Minimum Maximum Listing	SwissProt	No. is the m greater than s derived by a	- oke	군류	
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1_RAT P70553 rattus norv P30433 pongo pygma 7_CAMJE Q9pie4 campylobact C21515 phodopus su P4340 pongo pygma C9pie4 campylobact C21515 phodopus su P01732 homo sapien P33706 canis famil H_AGRTS Q44342 agrobacteril C000SI Q00825 chomo sapien P09326 homo sapien PNEIMA C99128 homo sapien PNEIMB C99128 homo sapien PNEIMB P09326 homo sapien PNEIMB P09326 homo sapien PNEIMB P09326 homo sapien PNEIMB P09326 homo sapien P09326 homo sapie	EMULT.  LEATHERAN STANDARD; PRT; 253 AA.  10.007-1998 (Rel. 34, Created) 10.007-1998 (Rel. 34, Last sequence update) 10.007-1998 (Rel. 34, Last sequence update) 10.007-1998 (Rel. 34, Last annocation update) 10.007-1999 (Rel. 35, Least annocation update) 10.007-1999 (Rel. 35, Rel.
NEM1 RAT CD8A_DONEY Y357_CAMDE NU4M_PHOSU CD8A_HUMAN CD8A_CANFA FLGH_AGRT5 FLGH_AGRT5 TRUE_NEIMA TRUE_NEIMB TRUE_NEIMB C559A_DROME	Created) Last sequence up Last sequence up Last annotation ( EEC 3.4.21) (  r (EEC 3.4.21) (  rordata; Craniata rimates; Catarrhi and characteriza (
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11 12 20 20 20 20 20 20 20 20 20 20 20 20 20	STANDARD;  1. 34, Created)  1. 34, Last see and ecursor (BC 3.4 Last and ecursor)  20a; Chordata; Tria; Primates;  7. AND SEQUEN  2. AND SEQUEN  3. AND SEQUEN  3. AND SEQUEN  4. AND SEQUEN  5. PubMed=8034;  6. PubMed=8034;  6. PubMed=11054  8. PubMed=11054  8. PubMed=11054  8. PubMed=11054  8. PubMed=11054  9. PubMed=11054  8. PubMed=11054  9. PubMed=11054  8. PubMed=11054  9. PubMed=11054  8. PubMed=11054  9. PubMed=11054  9. PubMed=11054  9. PubMed=11054  9. PubMed=11054  8. And
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	TIT 1  FUNDAN  KLEY HUMAN STANDARD,  P49862;  O1-OCT-1996 (Rel. 34, Ld.  O1-OCT-2003 (Rel. 42, Ld.  Allikrain 7 precursor  ENAINKERS OR SCCE.  Homo sapiens (Human).  EUKARYOCE, Metazoa (Cho)  MAMMABILIA EUCHERIA;  PRINCES OR SCCE.  Homo sapiens (Human).  EUKARYOCE, Metazoa (Cho)  NCHI TAXID-9606;  [1] — SEQUENCE FROM N.A., AND  TISSUE-SKIII,  MEDLINE-94308225; PubMec  Egglund T.;  "Cloning, expression, ar  Chymotryptic enzyme. A s  Gloning, expression, ar  Chymotryptic enzyme. A s  "Molecular Chem. 269:19422  [2]  SEQUENCE FROM N.A.  TISSUE-Rerainocytes;  YOUSE (G.M., SCOTILBS A.  "Molecular Characterizathuman stratum corneum of Submitted (BEC-1999) to  [3]  SEQUENCE FROM N.A.  "Molecular Characterizathuman stratum corneum of Submitted (BEC-1999) to  [4]  SEQUENCE FROM N.A.  "Moss P., Paeper B., Wang  "Sequencing and expression  "
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us-09-905-083-36.rsp

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus NCBL\_TaxID=10090,

SEQUENCE FROM N.A.

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RX SUCUENCE TRUE NO. 1.4.

EXTRAIN=57BL/661, TISSUB=Embryo;

EX MEDIINE=21085660; PubMed=11217851;

EX ARAMA J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishili Y.,

EX Arawa K., Ishawa M., Nishi K., Yoshono H., Adachi J., Fukuda S.,

EX Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

EX Asito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

EX Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

EX Radota K., Matsuda H.A., Oissi C., King B., Kochiwa H.,

EX Schimi L.M., Staubil F., Suruki R., Tomita M., Wagner L., Washio T.,

EX Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

EX Sakai K., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

EX Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

EX Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

EX Brownstein M.J., Bult C., Fletcher C., Fujita M., Monbaerts P.,

EX Brownstein M.J., Bult C., Seya T., Shipata Y., Storch K.-F.,

EX Brownstein H., Sato K., Schoenbach C., Seya T., Shipata Y., Storch K.-F.,

EX Brownstein H., Sato K., Kohoenbach C., Seya T., Shipata Y., Storch K.-F.,

EX Brownstein H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

EX Brownstein Y., Toyo-oka K., Habesgawa Y., Kawaji H., Kohtsuki S.,

EX Brownstein Y., Toyo-oka K., Habesgawa Y., Kawaji H., Kohtsuki S.,

EX Brownstein Y., Toyo-oka K., Habesgawa Y., Kawaji H., Kohtsuki S.,

EX Brownstein Y., Toyo-oka K., Hayshiazaki Y., Kawaji H., Kawaji H., Ruttaker C., Wilming L.,

EX Brownstein Y., Toyo-oka K., Hayshiazaki Y., Kawaji H., Kawaji H., Ruttaker Y.,

EX Brownstein Y., Ruttaki Y.,

EX Brownstein Y., Ruttaker C., Willwing L.,

EX Brownstein Y., Ruttaki Y.,

EX Brownstein Y.,

EX
           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNEL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-1-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to infiammarcry cytokines.

TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Very low levels are also seen in the brain and kidney.

SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IRRO01254; Peptidase all tresumentation, and interPro; IRRO01254; Peptidase S1.
InterPro; IRRO01254; Peptidase S1A.
InterPro; IRRO01214; Peptidase S1A.
Pram; PRO0089; LYPSBin, I.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS00240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Serine protease; Zymogen; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF166330; AAD49718.1; -.
EMBL; AF24527; AAG33360.1; -.
EMBL; AF32323 AAK69624.1; -.
EMBL; AF39328 A53968.
HSSP; P00763; IDPO.
MEROPS; S01.300; -.
MEROPS; S01.300; -.
GO; GO:0008236; F:serine-type peptidase activity; TAS.
GO; GO:0008236; F:serine-type peptidase.
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EMBL; AF166330; AAD49718.1; -.
EMBL; AF243527; AAG33360.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27525 MW;
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253 AA;
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUS=Mammary gland;

XX BEDINES-2138827; Pubmed=12477932,

XX STRAIN=C57BL/6J; TISSUS=Mammary gland;

XX STRAIN=C57BL/6J;

XX STRAIN=C57BL/6J;

XX STRAIN=C5.

XX STRAIN-C5.

XX STR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein synthesis.
-!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .: SIMILARITY: Belongs to the FKBP-type PPIase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK003331; BAB22719.1; --
EMBL; AK019132; BAB31559.1; --
EMBL; BC037596; AAH37596.1; --
HSSP; P20071; 1FKJ.
MGD; MGI:19313370; FKBP_11
InterPro; IPRO1179; FKBP_PPIASE.
PFAM; PF00224; FKBP; 1.
PROSITE; PS00453; FKBP_PPIASE_1; 1.
```

ö

Gaps

ö

4 SLLLPLQIL 12

1 SILLIPIQIL 9

FKII\_MOUSE STANDARD; PRT; 201 AA.
09DIM7; Q9CER4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
FK506 binding protein 11 precursor (EC 5.2.1.8) (Peptidyl-prolyl cistrans isomerase) (Rotamase) (Rotamase) (19 kDa FK506-binding protein)

FKBP11. Mus musculus (Mouse).

```
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein XAC1647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gamm.
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LLLPLQIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=92829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YG47 XANAC
Q8PLY8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
747 XANAC
100 YG47 XANAC
101 28-FEB
DT 28-FEB
D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vulpecula).";

J. Mol. Endocrinol. 21:141-152(1998)

-1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
INHIBINS/ACTIVINS ARE INVOLVED IN REGULARING A NUMBER OF DIVERSE FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION, GRAN CELL DEVELOPMENT AND MATURATION,
REXTHROLD DIFFERENTIATION, INSULIN SECRETION, NEXULE SURVEY CELL SURVITAL.
SUBBLY COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=99027340; PubMed=9801457; Vanmontfort D., Fidler A.E., Heath D.A., Lawrence S.B., Tisdall D.J., Vanmontfort D., McNatty K.; "cDNA sequence analysis, gene expression and protein localisation of the inhibin alpha subunit of Australian brushtail possum (Trichosurus
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trichosurus vulpecula (Brush-tailed possum).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Metatheria, Diprotodontia, Phalangeridae, Trichosurus.
                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVINS.
SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                PPIASE, FKBP-TYPE.
5 -> F (IN REF. 1, BAB31559).
5 -> R (IN REF. 1, BAB31559).
94D955C57264BD82 CRC64;
                                                                                                                                                                                                                               Score 34; DB 1; Length 201;
Pred. No. 8.3;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF03349; AAG3945.1; -. GO, GO:0005576; C:extracellular; ISS. GO; GO:0005576; C:extracellular; ISS. GO; GO:0007106; F:activin inhibitor activity; ISS. GO; GO:0005125; F:cytokine activity; ISS. GO; GO:000379; F:defense/immunity protein activity; ISS. GO; GO:0005179; F:brownh factor activity; ISS. GO; GO:0005179; F:brownh factor activity; ISS. GO; GO:0005515; F:protein binding; ISS. GO; GO:0007050; P:cell cycle arrest; ISS. GO; GO:0007050; P:cell differentiation; ISS.
                                                                       POTENTIAL. FK506 BINDING PROTEIN 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2001 (Rel. 40, Last annotation update)
Inhibin alpha chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 AA
PROSITE; PS00454; FKBP PPIASE 2; FALSE_NEG.
PROSITE; PS50059; FKBP PPIASE_3; 1.
ISOMETASE; Rotamase; Signal.
CHAIN
28 201 PK506 BINDING
                                                                                          28 201 FK
57 144 PP
53 53 5
198 198 S
201 AA; 22137 MW;
                                                                                                                                                                                                                                 Query Match 85.0%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                           6 LLLPLOLL 13
                                                                                                                                                                                                                                                                                                                               2 LLLPLQIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IHA TRIVU
                                                                                                                DOMAIN
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
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GO; GO:0008151; P:cell growth and/or maintenance; ISS.
GO; GO:0007565; P:cell surface receptor linked signal transdu. .; ISS.
BR GO; GO:0007267; P:cell-cell signaling; ISS.
BR GO; GO:0007267; P:cell-cell signaling; ISS.
BR GO; GO:000517; P:hemoglobin biosynthesis; ISS.
BR GO; GO:006517; P:hemoglive regulation of follicle-stimulating. .; ISS.
BR GO; GO:0045578; P:hemoglive regulation of follicle-stimulating. .; ISS.
BR GO; GO:004226; P:hemoglive regulation of phosphorylation; ISS.
BR GO; GO:004226; P:hemoglive regulation of phosphorylation; ISS.
BR GO; GO:0045817; P:hemoglive regulation of phosphorylation; ISS.
BR GO; GO:0046881; P:hemoglive regulation of phosphorylation; ISS.
BR GO; GO:0046881; P:hemoglive regulation of follicle-stimulating. .; ISS.
BR GO; GO:0046881; P:hemoglive regulation of follicle-stimulating. .; ISS.
BR THEFPC; IPRO0189; TGFb.
BR PRINTS; PRO0199; TGF-beta; I.
BR PRINTS; PRO0199; TGF-beta; I.
BR PROSITE; PRO0269; TGF-BETA_1; I.
BR SMART; SMO0204; TGFB; I.
BR SIMILARILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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SEQUENCE FROM N.A.

CARAIN=306 / ATCC 13902 / XV 101;

MEDLINE=2202145; PubMed=12024217;

Ad Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A lose L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

A lose L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Ratia J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Ratia J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Antinis E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira W.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
BY SIMILARITY.
INNIBIN ALPHA CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 1; Length 361;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38945 MW; D661CDF93CDAA87D CRC64;
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**AAAHHHOOOOOOOOOAKK** 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/6J; TISSUD=Head;

STRAIN-C57BL/6J; TISSUD=Head;

MICHINE-22354683; PubMed=12466851;

MICHARDINE-22354683; PubMed=12466851;

MICHARDINE-22354683; PubMed=12466851;

MICHARDINE-22354683; PubMed=12466851;

MICHARDINE, N. FABRAWA T., AGGAMI H., Kondos, S., Andarelli R., Hill D.P., Bult C., Hume D.A., Ounckenbush J., Baldarelli R., Hill D.P., Bult C., Hume D.A., Dackenbush J., Baldarelli R., Frazer K.S., Baldarelli R., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Cousins S., A Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Kanai A., Kawaji H., Marchionni L., McKenzie L., Miki H., Magashima T., Numata K., Pontius J.U., Qi D., Farned G., Pescle G., Pescle G., Pescle G., Pescle G., Pescle G., Setou M., Shimad K., Sandelin A., Schoneider C., Semple C.A., Setou M., Shimad K., Verlack R., Wahnestedt C., Wang Y., Waranabe Y., Wallsing L.G., Wahnestedt C., Wang Y., Waranabe Y., Wang I., Yang I., Yang I., Yang I., Yang I., Yang I., Xun Z., Zavolan M., Zanolan M., Sato K., Hirozane-Kishikawa T., Nunkamura M., Sakazume N., Sato K.,
Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P.; "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
EMILIN 1 precursor (Elastin microfibril interface-located protein 1)
EMILIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 1; Length 339;
Pred. No. 22;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                          HAMAP, MF_01206; -; 1.
InterPro; IPR000572; Oxidored_molyb.
InterPro; IPR006311; Tat.
Pfam; PF00174; oxidored_molyb; 1.
ITGREAGA; TGR01409; TAT signal, seq; 1.
Hypothetical protein; Complete protecome.
SEQUENCE 339 AA; 37901 MW; B926DFC9AAB49438 CRC64;
                                                                                                     Nature 417:459-463(2002).
-!- SIMILARITY: Belongs to the UPF0190 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1017 AA
                                                                                                                                                                                                                                                                                                        EMBL; AE011796; AAM36515.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLLLPLOPL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SLLLPLQIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MI1_MOUSE
D _EMI1_MOUSE
C Q99K41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESULT 5
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REPEZIOPMENTAL STAGE.

REPEZIONE DEVELORMENTAL STAGE.

REPEZIONE STAGE.

REPZIONE STAGE.

REP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold B.A., Grouse L.H., Schaefer C.F., Shuler G.D.,
Altschul S.F., Zeeberg B.B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninol P., Frange C.,
Raha S.S., Loquellano M.A., Perers G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Alichards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Antiting M., Touchman J.W., Green B.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smailus D.E.,
M. Schnerth A., Schein J.B., Jones S.J.M., Marra M.A.;
""Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., Materston R., Lander E.S., Rogers J., Maraysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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succinoglycan biosynthesis.";
J. Bacteriol. 175:7045-7055(1993).
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                                      STRAIN=1021;
MEDLINE=94042870; PubMed=8226646;
Glucksmann M.A., Reuber T.L., Walker G.C.;
"Genes needed for the modification, polymerization, export, and processing of succinoglycan by Rhizobium meliloti: a model for
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"Family of glycosyl transferases needed for the synthesis of
succinoglycan by Rhizobium meliloti.";
J. Bacteriol, 175:7033-7044(1993)
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01-FBB-1994 (Rel. 28, Last sequence update)
01-FBB-1994 (Rel. 28, Last sequence update)
01-FBB-1994 (Rel. 24, Last annotation update)
Succinoglycan biosynthesis transport protein exoT.
EXOT OR RB1074 OR SMB20950.
EXOT OR RB1074 OR SMB20950.
Flainzobium meliloti (Sinorhizobium meliloti).
Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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Pred. No. 66;
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MEDLINE=94042869; PubMed=8226645;
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                                                                                                           "Analysis of the Rhizobium meliloti genes exoU, exoW, exoW, and exoI involved in exopolysaccharide biosynthesis and nodule invasion: exoI and exoW probably encode glucosyltransferases.";

Mol. Plant Microbe Interact. 6:735-744 [1993].
                                                                                                                                                                                                                                                                                      Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P., Finan T.M., Weidner S., Mong K., Buhrmester J., Chain P., Vorhoelter F.W., Weidner S., Wong K., Becker A., Cowie A., Gouzy J., Golding B., Puehler A.;

"The complete sequence of the 1,633-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinopium meliloci.";

Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).

-!- PATHWAY: Exopolyyaaccharide biosynthesis a PATHWAY: LOCATION: Integral membrane protein (Probable).

-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
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SEQUENCE FROM N.A.
STRAIN=RCR2011 / S147;
MEDLINE-94162682: PubMed=8118055;
Becker A., Kleickmann A., Kuester H., Keller M., Arnold W.,
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Pred. No. 52;
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Exopolysaccharide synthesis; Transmembrane; Plasmid;
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ID CUTI BOTCI STANDARD; PRT; 202 AA. AC Q00298; DT 01-NOV-1997 (Rel. 35, Last sequence update)
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PIR; B95976; B95976.
PIR; C49349; C49349.
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TISSUES Salivary gland;

MEDINELS 288257; PubMed=12477932;

MEDINELS 288257; PubMed=12477932;

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                                                                                                                                                                                                                                                                                                                                     Mawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., A Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S., Alaxawa T., Izawa M., Nishi Y., Kiyosawa H., Kondo S., Yamanaka I., Baito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Mashio T., Sakai K., Okido T., Furuno M., Aon H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Ashinci P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ringwald M., Rodriguez I., Sakamoto N., Assaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whittaker C., Whittaker C., Wilming L., Wanshaw-Bootis A., Voshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                 Inoue S., Sano H., Ohta M., "Group strong the superstion of Expression of "Growth suppression of Escherichia coli by induction of expression of mammailan genes with transmembrane or ATPsase domains."; edochem. Biophys. Res. Commun. 268:553-561 (2000)
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-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Contains 1 ubiquitin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/60; TISSUE=Small intestine;
MEDLINE=21095660; PubMed=11217851;
                                                                                        MEDLINE=20145471; PubMed=10679242;
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EMBL; AK008109; BAB25465.1; -.
EMBL; BC019547; AAH19547.1; -.
MGD; MGI:1923764; 2010004020Rik.
INCEPPC; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin.
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                               FROM N.A.
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                                                                                                                                                                                mammalian
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van der Vlugt-Bergmans C.J.B., Wagemakers L.C.A.M., van Kan J.A.L.;
"Cloning and expression of the cutinase A gene of Botrytis cinerea.";
Mol. Plant Microbe Interact. 10.21-29/1997).
-!-FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that forms the structure of plant cuticle. Allows pathogenic fungi to penetrace through the cuticular barrier into the host plant during the initial stage of the fungal infection (By similarity).
-!-CATALYTIC ACTIVITY: Cutin + H(2)0 = cutin monomers.
-!-SUBCELLULAR LOCATION: Secreted (By similarity).
-!-THM: The 2 disulfide bonds play a critical role in holding the catalytic residues in luxta-position; reduction of the disulfide bridges results in the complete inactivation of the enzyme (By
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                  CUTA.

Botrytis cinerea (Noble rot fungus) (Botryotinia fuckeliana).

Butrytis cinerea (Noble rot fungus) (Botryotinia, Eotiomycetes;

Butryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;

NCBI_TaxID=40559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.5%; Score 31; DB 1; Length 202; 66.7%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             031D64725A23D8E7 CRC64;
10-OCT-2003 (Rel. 42, Last annotation update) Cutinase precursor (EC 3.1.1.74) (Cutin hydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SIMILARITY: Belongs to the cutinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUTINASE.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000675; Cutinase.
Pfam; PF01083; Cutinase; 1.
PRINTS; PR00129; CUTINASE.
PROSITE; PS00155; CUTINASE 1; 1.
PROSITE; PS0931; CUTINASE 2; 1.
Hydrolase; Serine esterase; Signal.
SIGNAL
                                                                                                                                                                                                                                                               STRAIN=SAS56;
MEDLINE=97155570; PubMed=9002269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20253 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z69264; CAA93255.1; -.
HSSP; P00590; 1XZJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein Clorf21 homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202
172
165
165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31
106
117
169
182
202 AA;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
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Q9JMG3; G21\_MOUSE ESULT 8

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GPDA_TRYBB
P90593;
                                                                                                                                                                                                              DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                       TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                       TRANSMEM
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GPDA_TRYBB
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Kidney, and Placenta;

TISSUE-Kidney, and Placenta;

TISSUE-Kidney, and Placenta;

MEDINE-228825; PubMed=1247932;

Attausher R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Attachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Appleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Brownstein M.J., Uddin T.B., Tonbhyuki S. Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wakernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Allalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S., Morley W., Schermen M., Nadan A., Rodrigues S., Sanchez A.

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myerz M.A.,

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.,

Rutterfield Y.S.N., Varywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myerz R.M.,

Rutterfield Y.S.N., Varywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.,

Rutterfield Y.S.N., Varywinski M.I., Skalska U., Smailus M.A.,

Rutterfield Y.S.N., Varywinski M.I., Skalska U., Smailus M.A.,

Rutterfield Y.S.N., Starywinski M.I., Skalska U., Smailus M.A.,

Rutterfield Y. S. Schmutz J., Schola W.A.,

Rutterfield Y. S. Schola W. Schola W. S., Schola W. S., Schola W. S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Contains 1 ubiquitin-like domain.
                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                  Score 31; DB 1; Length 245;
Pred. No. 42;
1; Mismatches 1; Indels
                                                                                         POTENTIAL.
POTENTIAL.
UBIQUITIN-LIKE.
LEU-RICH.
#, 02CID1B24C13139D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang W., Li N., Wan T., Zhang M., Cao X.,
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein C70rf21 (SB144)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                       POTENTIAL
                    PROSITE; PS50053; UBIQUITIN_2; 1.
Transmembrane.
                                                                  11 31 POT
194 214 POT
219 239 POT
102 175 UBI
197 238 LEU
245 AA; 26316 MW; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY037155; AAK67645.1; -. EMBL; BC000936; AAH00936.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
UBQ; 1.
                                                                                                                                                                                                                                                                                                                                                                               196 SLLEPLLL 204
                                                                                                                                                                                                                                                                                                                                   1 STITESTOIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
  SMART; SM00213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CG21 HUMAN
                                                                    TRANSMEM
TRANSMEM
TRANSMEM
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trypanosoma brucei brucei.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE-27077437; PubMed-8920004;

Kohl L., Drmota T., Thi C.D., Callens M., van Beeumen J.,

Opperdoes F.R., Michels P.A.M.;

"Cloning and characterization of the NAD-linked glycerol-3-phosphate
dehydrogenases of Trypanosoma brucei brucei and Leishmania mexicana
mexicana and expression of the trypanosome enzyme in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOI. Biochem. Parasitol. 76:159-173(1996).
-!- CATALYTIC ACTYVITY: Sn-glycerol 3-phosphate + NAD(+) = glycerone
--- phosphate + NADH.
--- STBCELLUIAR LOCATION: Glycosomal.
--- SIMILARITY: Belongs to the NAD-dependent glycerol-3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MICROBODY TARGETING SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-MAY-2004 (Rel. 43, Last amnotation update)
Glycerol-3-phosphate dehydrogenase [NAD+], glycosomal (EC 1.11.8).
                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                      Score 31; DB 1; Length 246;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                            UBIQUITIN-LIKE.
LEU-RICH.
BO8E25A6B37665B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37783 MW; 12CE19AEDA9E4EC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 AA
                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 42;
1; Mismatches
                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IRR008927; 6DGDH C like.
InterPro; IRR006168; NAD GIy3P dh.
InterPro; IRR006109; NAD GIy3P dm.
Pfam; PF01210; NAD GIY3P di; 1.
RINTS; PR00077; GFDHDRGNASE,
ProDom; PD001278; NAD GIy3P dom; 1.
PROSITE; PS00957; NAD GIY3P dom; 1.
EMBL; BC033182; AAH33182.1; -. Genew; HGNC:21709; C7orf21.
InterPro; IPR00626; Ubiquitin.
Efam; PF00240; ubiquitin; 1.
PROSITE; PS50053; UBIQUITIN_2; 1.
Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; NAD; Glycosome
                                                                                                                                                                                                                                                                                                     26261 MW;
                                                                                                                                                                                                                                                                                                                                                   77.5%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X89738; CAA61890.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                 31
215
241
176
239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 SLLLPLLL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SLLLPLQIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; T48649; T48649.
                                                                                                                                                                                           195
221
221
203
198
246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Length 354;

77.5%; Score 31; DB 1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ViTat 1.1;
MEDLINES=7077436; PubMed=8920003;
Stebeck C.E., Prevert U., Mommeen T.P., Vassella E., Roditi I.,
Pearson T.W.;
"Molecular characterization of glycosomal NAD(+)-dependent glycerol 3-
phosphate dehydrogenase from Trypanosoma brucei rhodesiense.";
Mol. Biochem. Parasitol. 76:145-158(1996).
-!- CATALYTIC ACTIVITY: Sn-glycerol 3-phosphate + NAD(+) = glycerone
                                                                                                                                                                                                                                                                                                                                                                                                                     Trypanosoma brucei rhodesiense.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=31286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MICROBODY TARGETING SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                        phosphate + NADH.
-!- SUBCELLULAR LOCATION: Glycosomal.
-!- SUBCELLULAR LOCATION: Glycosomal.
-!- SIMILARITY: Belongs to the NAD-dependent glycerol-3-phosphate dehydrogenase family.
                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 AA; 37834 MW; OCE049CSE8F83C00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESULT 12
FUD ECOLI STANDARD; PRT; 428 AA.
C PYFUD ECOLI STANDARD; PRT; 428 AA.
C PSTANDES, P76600; P76601; P77009;
I 01-0CT-1994 (Rel. 30, Created)
I 15-DEC-1998 (Rel. 30, Last sequence update)
I 16-0CT-2001 (Rel. 40, Last annotation update)
S Hypothetical protein yfjD.
N YFUD OR B2612/B2613.
                                                                                                                                                                                                                                                            354 AA.
                              Mismatches
  Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X91142; CAA62581.1; -.
InterPro; IPR00827; 6DGDH C like.
InterPro; IPR006168; NAD GJ97B dh.
InterPro; IPR006109; NAD GJ97B dh.
InterPro; IPR006109; NAD GJ97B dh.
Pfam; PF01210; NAD GJ97P dh; 1.
ProDom; PD001278; NAD GJ97B dom; 1.
PROSITE; PS00957; NAD GJ97BH; 1.
Oxidoreductase; NAD; GJycosome.
                        0;
  77.8%;
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354
                                                                                                                          124 ŚLLFPAQIL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLLFPAQIL 132
                                                                          1 SLLLPLQIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase; NAD;
SITE 352 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STITTLETOID 9
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            TRYBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
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                                                                                                                                                                                                                                                                                       MEDIINE=97349980; PubMed=9205837; MEDIINE=97349980; PubMed=9205837; MEDIINE=97349980; PubMed=9205837; Makino K., Miki T., Aiba H., Baba T., Hayashi K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Uchara K., Wada C., Yamagata S., Horiuchi T.; "Construction of a contiguous 874-kb sequence of the Escherichia coli-ril general corresponding to 50.0-68.8 min on the linkage map and malysis of its sequence features.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipinska B., King J., Ang D., Georgopoulos C.; "Sequence analysis and transcriptional regulation of the Escherichia coli grpE gene, encoding a heat shock protein."; Nucleic Acids Res. 16:7545-7562(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: CONTAINS 2 CBS domains.
-1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 199 THAT PRODUCES TWO ORFS.
-1- CAUTION: Ref.3 sequence differs from that shown due to numerous frameshifts.
                                                                                                  STEALN=X12 / MG1655;
MEDLINE=27426617; PubMed=9278503;
MEDLINE=97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Gregor J., Shao Y.;
                   Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- SIMILARITY: BELONGS TO THE UPF0053 FAMILY. STRONG, TO
H.INFLUENZAE H10107.
                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain; Repeat; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000347; AAC75661.1; ALT FRAME.
EMBL; AE000347; AAC75662.1; ALT FRAME.
EMBL; X07863; -; NOT ANNOTATED_CDS.
ECGENE; EG12443; yffD.
INCEPPO; IRROSCESO, CBS.
INTERPO; IRROSCESO, CBS.
INTERPO; IRROSCESO, COC_LYANSPLATED_CDS.
FAM: PF00571; CBS.
FAM: PF00571; CBS.
FAM: PF00571; COC_LYANSPLATED_CDS.
Pfam: PF01595; DUF2T; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rudd K.E.;
Unpublished observations (AUG-1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=88319942; PubMed=3045760;
                 Bacteria, Proteobacteria, Gammar
Enterobacteríaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 322-428 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00116; CBS; 1.
Hypothetical protein; CBS
Complete proteome. 4
TRANSMEM 65 85
                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                     NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION.
                                                                                      SEQUENCE
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IL2 BOVIN
P05016;
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MOD RES
SEQUENCE
                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                RESULT 14
IL2_BOVIN
ID _ IL2 Po
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mes by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acd. Sci. U.S.A. 89:5877-5881(1992).

-!- FUNCTION: Brings about phosphorylation of specific threonines in the heavy chains of myosin during chemotaxis, which results in inhibition of myosin thick filament formation. Phosphorylation also inhibits the actin-activated ATPase activity of myosin.

-!- CATALYTIC ACTIVITY: ATP + [myosin heavy-chain] = ADP + [myosin heavy-chain] phosphate.

-!- SUBCELLUAR LOCATION: Membrane-bound.

-!- DEVELOPMENTAL STAGE: Expressed only during development.

-!- SIMILARITY: Belongs to the eukaryotic diacylglycerol kinase
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92335200; PubMed=1321427;
Ravid S., Spudich J.A.;
"Membrane-bound Dictyostelium myosin heavy chain kinase: a
developmentally regulated substrate-specific member of the protein
kinase C family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG binding domains.
-!- CAUTION: While this is experimentally defined to be a protein kinase, it could be, on the basis of sequence similarities, a diacylglycerol kinase.
                                                                              ö
                                                77.5%; Score 31; DB 1; Length 428; 87.5%; Pred. No. 72; cive 0; Mismatches 1; Indels
             POTENTIAL.
38456865EDBCB151 CRC64;
                                                                                                                                                                                                                                                                                   Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Myosin heavy chain kinase (EC 2.7.1.129) (MHCK).
                                                                                                                                                                                                783 AA
  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P04049; IFAR.
DictyBase; DDB0165000; M93393.
DictyBase; DDB016500019; DAG PE-bind.
InterPro; IPR000705; DAGKa.
InterPro; IPR001206; DAGKc.
Pfam; PF00130; DAG PE-bind; 1.
Pfam; PF00609; DAGKa: 1.
                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M93393; -; NOT ANNOTATED CDS
PIR; A46136; A46136.
 92 112 PC
130 150 PC
428 AA; 48044 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD002939; DAGKa; 1.
ProDom; PD005043; DAGKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00109; C1; 2.
SMART; SM00045; DAGKa; 1.
SMART; SM00046; DAGKC; 1.
                                                                               Conservative
                                                                                                                                                                                                STANDARD;
                                                                                                                                  131 LLAPLOIL 138
                                                                                                       2 Librardi 9
                                                   Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                               KWHC DICDI
P34125;
01-FEB-1994 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family
               TRANSMEM
SEQUENCE
  TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                            PHOSPHORYLATION (AUTO-) (BY SIMILARITY). 6CAF177F4436F43E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cerretti D.P., McKereghan K., Larsen A., Cantrell M.A., Anderson D., Gillis S., Cosman D., Baker P.E., "Cloning, sequence, and expression of bovine interleukin 2.", Proc. Natl. Acad. Sci. U.S.A. 83:3223-3227(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.

PROSITE; PS50081; DAG PE_BIND_DOM_2; 2.

Transferame; Serine/Lhreonine-profein kinase; ATP-binding; Membrane; Phosphorylation; Phorbol-ester binding; Repeat.

DOMAIN 19 69 PHORBOL-ESTER AND DAG BINDING 1.

PHORBOL-ESTER AND DAG BINDING 2.

PHORBOL STREAM ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILZ OR IL-2.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=86205870; Pubmed=3486415;
Reeves R., Spies A.G., Nissen M.S., Buck C.D., Weinberg A.D.,
Barr P.J., Magnuson N.S., Magnuson J.A.;
"Molecular cloning of a functional bovine interleukin 2 cDNA.";
Proc. Natl. Acad. Sci. U.S.A. 83:3228-3232(1986).
                                                                                                                                                                                                                                                                                                                                                                                            .
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13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TGF)
                                                                                                                                                                                                                                                                                                                                     Score 31; DB 1; Length 783;
Pred. No. 1.3e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 AA
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SER/THR-RICH.
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EMBL; M13204; AAA21143.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=86205869; PubMed=3517854;
                                                                                                                                                                                                                                                                                           89154 MW;
                                                                                                                                                                                                                                                                                                                                          77.5%;
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                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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138
474
489
196
773
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                                                                                                                                                                                                                188
754
768
783 AA;
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Bur. V. Immunogenet. 29:341-345(2002).

-i- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine activated killer cells, natural killer cells, and glioma cells (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDNed=12121282; MEDIINE=22117321; PubNed=12121282; Sreekumar E., Premraf A., Saravanakumar M., Rasool T.J.; Sreekumar E., Premraf A., Saravanakumar E., sequence analysis reveals "Buffalo (Bubalus bubalis) interleukin-2: sequence analysis reveals high nucleotide and amino acid identity with interleukin-2 of cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                INTERLEUKIN-2.
BY SIMILARITY.
O-LINKED (GALLAC. . .) (BY SIMILARITY).
- A (IN REF. 2).
816667DFEA052EDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bubalus bubalis (Domestic water buffalo).
Sukaryotas Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bubalus.
EMEL, X52687; CAA36912.1; -...
PIR; 145913; 145913.
HSSP, P01585; 31NK.
InterPro; IRF00079; Interleukin-2.
PRINTS; PRO0755; INTERLEUKIN2.
PRINTS; PRO0265; INTERLEUKIN2.
PROSITE; PSO0424; INTERLEUKIN2.
PROSITE; PSO0424; INTERLEUKIN 2; 1.
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TGGF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.0%; Score 30; DB 1; Length 155; 77.8%; Pred. No. 43; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF363786; AAK50039.1; -.
InterPro; IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
PRINTS; PR00265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
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21 155 IW
79 127 BY
23 0-1
66 66 V V
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Best Local Similarity 77.8
Matches 7; Conservative
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Q95KP3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                    (BY SIMILARITY)
PROSITE; PS00424; INTERLEUKIN_2; 1.
Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
                                                                                                                             ö
                                                                                                    75.0%; Score 30; DB 1; Length 155; 77.8%; Pred. No. 43; tive 1; Mismatches 1; Indels
                                 BY SIMILARITY.
INTERLEUKIN-2.
BY SIMILARITY.
O-LINED (GALWAC. ..) (BY
#, 1753173FE619946B CRC64;
                                                                                                                                                                                                          Search completed: March 1, 2004, 17:29:59 Job time: 7 secs
                                1 20 BY
21 155 INT
79 127 BY
23 23 0-1
155 AA; 17541 MW;
                                                                                                                              Conservative
                                                                                                                                                                            44
                                                                                          Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                    1 SLLLPLOIL
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                                                         DISULFID
                                                                                  SEQUENCE
                           -cell
                                     SIGNAL
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emericella mus musculu

Q92255 mus musculu Q92255 mus musculu Q98162 agrobacteri Q98162 attus norv Q9m0j5 arabidopsis Q86166 porphyromon Q8214 streptomyc Q9630 giardia lam Q98x56 arabidopsis Q9119 homo sapien Q98x16 arabidopsis Q9119 homo sapien Q98x66 arathomonas Q98x66 xanthomonas Q98x66 yarobaculum Q98x16 yarobaculum

Q9vyn0 drosophila Qx620 salmonella O76155 periplaneta Q84bf5 xanthomonas Q8wx77 homo sapien O22910 arabidopsis

Q8u6y8 agrobacteri Q82vh0 nitrosomona Q9kal1 bacillus ha P96675 bacillus su

Q9v3y4 drosophila Q9mms8 syrigma sib

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Gaps

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Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 40; DB 4; Length 253; 100.0%; Pred. No. 3.7; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO: GO: 0004223; F: chymotrypsin activity; IEA.
GO: GO: 0004233; F: peptidase activity; IEA.
GO: GO: 0004235; F: trypain activity; IEA.
GO: GO: 0004255; F: trypain activity; IEA.
GO: GO: 0005259; F: trypain activity; IEA.
GO: GO: 0005259; F: trypain activity; IEA.
InterPro: IPR009003; Cyg Ser_trypsin.
InterPro: IPR001254; Peptidase_S1.
R PRINTS; PR001254; Peptidase_S1A.
R PRINTS; PR00125; CHYMOTRYPSIN.
SWART; SM00020; Tryp SFC; 1.
R PROSITE; PS00134; TRYPSIN_DOM; 1.
R PROSITE; PS00135; TRYPSIN_DOM; 1.
R PROSITE; PS00135; TRYPSIN_DOM; 1.
R PROSITE; PS00135; TRYPSIN_ER: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Strausberg R.; Strausberg (1978) to the EMBL/GenBank/DDBJ databases. Submithed (JUN-2002) to PEPTIDASE FAMILY SI. EMBL; BC032005; AAH32005.1;
                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Kallikrein 7 (chymotryptic, stratum corneum)
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                           ALIGNMENTS
                       Q9ESS3
035426
09R184
09M0J5
086166
                                                                                                                             Q9P1I9
Q8PKF6
Q8ZUD7
                                                                                                            OSFL49
OBLWX9
                                                                                                                                                                                                                                           082VH0
09KAL1
P96675
                                                                                                                                                                                                         022910
                                                                                                                                                                                                                                    QBUGY8
                                                                                                    OBRX56
                                                                                                                                                                             076155
Q84BF5
Q8WX77
                                                                                Q12212
Q969D0
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                                                                                                                                                          Q9VYN0
                                                                                                                                                                                                                 09V3Y4
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8 110
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Matches 9, Conserv
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TISSUE=Skin;
NCBI_TaxID=9606;
Query Match
                                                                                                                                                                                                                                                                                                                                          Q8N5N9
                                                                                                                                                                                                                                                                                                                      RESULT 1
QBN5N9
 Q8vca9 mus musculu Q8r5d6 mus musculu Q8r5d6 mus musculu Q8r5d5 brucella me Q8f2x1 brucella su Q7u3j6 synechococo Q7v4d prochloroco Q819m8 bacillus ce Q8vbb6 white spot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7u5r4 synechococc
Q9d226 mus musculu
Q9zte3 arabidopsis
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Q8brv0 mus musculı
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O21527 clethrionom
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                                                               March 1, 2004, 17:20:41; Search time 30.3333 Seconds (without alignments) 93.615 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
         GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                        otal number of hits satisfying chosen parameters:
                                                                                                                                                                       1017041 segs, 315518202 residues
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                                               sw model
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Q9V2DS
Q9V2DS
Q8VCA9
Q8RYD9
Q8FX10
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sp_bhage:*
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sp_rodent:*
sp_virus:*
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sp_vortebrate:*
sp_molassified:*
sp_roforce.*
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Gapop 10.0 , Gapext 0.5
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sp_mammal:*
sp_mhc:*
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Maximum Match 100%
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sp_bacteria:*
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seq length: 200000000
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Match Length DB
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sp_human:*
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Q8R5D6
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QBVCA9
ID QBVC
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-1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

-1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

-1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

-1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.

GO; GO:0008137; F:NADH dehydrogenase activity; IEA.

GO; GO:0006120; F:NALOGNORATAL electron transport, NADH to u. .; IEA.

InterPro; IPR00350; Oxidored_G1.

InterPro; IPR000260; Oxidored_G1.

InterPro; IPR000260; Oxidored_G2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Pyrococus abyssi genome sequence: insights into archaeal chromosome structure and evolution "; Submitted (ULL-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AJ748283; CA449063.1; -. PIR; H75201; H75201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;
"Molecular systematics and paleobiogeography of the South American
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clethrionomys gapperi (Southern red-backed vole).
Mitochondrion.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Arvicolinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN.1998 (TrEMBLrel. 05, Created)
01-JAN.1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
0x1-Cotagenase subunit 4 (EC 1.6.5.3) (NADH-ubiquinone oxidoreductase chain 4) (Fragment).
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                                                                                                                                                                                                                                                                                     O9V2D5,
O1-MAY-2000 (TEXMBLrel. 13, Created)
O1-MAY-2000 (TEXMBLrel. 13, Last sequence update)
O1-OCT-2003 (TEXMBLrel. 25, Last amoctation update)
Pypochetical protein PYRAB01390.
PYRAB01390 OR PAB0088.
                                                                                                                                                                                                                                                                146 AA
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Matches 8; Conservative
                                                                                                                                                                                                                                                            PRELIMINARY;
                                            4 SLLLPLOIL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 SLLLPLQII 74
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1 STITTBIOIT 9
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STRAIN=GE5 / Orsay;
Heilig R.;
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NCBI_TaxID=56223;
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NCBI_TaxID=29292;
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9V2D5
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Pred. No. 20;
1; Mismatches 0; Indels
                                                                                                                                                                    Query Match 92.5%; Score 37; DB 8; Length 208; Best Local Similarity 88.9%; Pred. No. 13; Matches 8; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; 2012 to the EMBL/GenBank/DDBJ databases. Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC021345; AAH31345.1; - SEQUENCE 73 AA; 7819 MW; 93E8F53399BF3C11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases EMBL; BCO22900; AAH22900.1; -. MGD; MGI:1913370; Fkbp11.
Pfam; PF00361; oxidored_q1; 1.
Pfam; PF01059; oxidored_q5 N; 1.
PRINTS; PR01437; NUOXDRDTASE4.
NAD; Oxidoreductae; Ubiquinone; Mitochondrion.
NON TER 208 208
SEQÜENCE 208 AA; 23967 MW; BAF1788697AED6A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
similar to RIKEN CDNA 1110002023 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-000-2002 (TrEMBLrel. 21, Created)
01-00N-2002 (TrEMBLrel. 21, Last sequence update)
01-00N-2003 (TrEMBLrel. 24, Last annotation update)
Similar to RIKEN cDNA 1110002023 gene.
FKBP11 OR 1110002023RIK.
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87.5%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 AA
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InterPro, IPR001179; FKBP_PPIase.
PROMITE, PS00453; FKBP_PPIASE 1; 1.
PROSITE; PS00453; FKBP_PPIASE 1; 1.
SEQUENCE 104 AA; 11085 MW; 0534D576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Best Local Similarity 87.33,
Best-Lac 7; Conservative
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                                                                                                                                                                                                                                                                                                     97 SLLVPLQIL 105
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TISSUE=Salivary gland;
                                                                                                                                                                                                                                                                             1 SLLLPLQIL 9
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Best Local Similarity
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PRT;
                                                                                                                            82.5%;
                                                                                              Query Match
Best Local Similarity 75...
6; Conservative
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PIR; AB3334; AB3334.
TIGR; BR1349; -.
Complete proteome.
SEQUENCE 370 AA; 4
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Q7U9J6;
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MEDLINE-20020109; PubMed=11756688;
MEDLINE-20020109; PubMed=11756688;
Delivecchio 'G', Kapadral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
"The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
EMBL, AE009507; AAL51837.1; -.
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     Gaps
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Brucellaceae, Brucella.
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Brucellaceae, Brucella.
NCBI_TaxID=29461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 370;
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                                                                                                                                                                                                                                                    01-MAR-2002 (TrEWBLrel. 20, Created)
01-MAR-2002 (TrEWBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Daunorubicin resistance transmembrane protein.
BMEI0556.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
ABC transporter, permease protein, putative.
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Pred. No. 1.4e+02;
2; Mismatches 0;
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     1; Mismatches
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MEDLINE=22247741; PubMed=12271122;
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     7; Conservative
                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                       6 LLLPLOLL 13
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                                                   LLLPLQIL 9
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Best Local Similarity
Matches 6; Conserv
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SEQUENCE 370 AA
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     Matches
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Palenik B., Brahameha B., Lariner F.W., Land M., Hauser L., Chain P.,
Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,
Dufresne A., Partensky F., Webb E.A., Waterbury J.;
"The genome of a montile marine Synechococcus.";
Mature 424:1037-1042(200)
EMBL; BX569689; CAE06775.1; -
Glycosyltransferase; Signal; Transferase; Complete proteome.
SIGNAL
SIGNAL
19 Potential.
SEQUENCE 379 AA, 40174 MW; 98D697ECEF71C73F CRC64;
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                                               Length 370;
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                                                               Score 33; DB 16; Length 37
Pred. No. 1.4e+02;
2; Mismatches 0; Indels
40369 MW; 819AAD684305CB60 CRC64;
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Q7V4U4;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glycosyl transferase, family 4 precursor (BC 2.4.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrels 25, Last annotation update)
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ESULT 10

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MEDLINE=21548311; PubMed=11689662; Yeard F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.; Complete genome sequence of the shrimp white spot bacilliform
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0; Mismatches
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                                                             Virol. 75:11811-11820(2001)
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Best Local Similarity 10v...
7; Conservative
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                                                  virus."
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Matches
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GO; GO:0016202; C:membrane; IEA.
GO; GO:0005311; F:godium:dicarboxylate/tricarboxylate symport. . .; IEA.
GO; GO:00005311; F:sodium:dicarboxylate/tricarboxylate symport. . .; IEA.
GO; GO:0000835; P:dicarboxylic acid transport; IEA.
InterPro; IPR001981; Call cycle.
InterPro; IPR001981; Na/dicO symport.
InterPro; IPR001981; Na/dicO symport.
PROSITE; PS00428; FTSW RODA SPOVE; 1.
PROSITE; PS00428; FTSW RODA SPOVE; 1.
PROSITE; PS00428; FTSW RODA SPOVE; 1.
CG11 division; Complete proteome.
SEQUENCE 392 AA; 42797 MW; 7AAAS8737762F659 CRC64;
                                                                                             Gaps
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MEDINE=2260415; PubMed=12721630;
MEDINE=2260415; PubMed=12721630;
Xapatral V., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Golteman B., Larsen N., D'Souza M., Walunas T.,
Carchkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
"Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
Nature 423:87-91(2003).
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   Glycosyltransferase; Signal; Transferase; Complete proteome.
SIGNAL 1 19 Potential.
SEQUENCE 381 AA; 40217 MW; 4DBAB55F313F8BEZ CRC64;
                                                               Length 381;
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                                                             Score 33; DB 16; Length 38
Pred. No. 1.5e+02;
0; Mismatches 1; Indels
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0819M8;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
6211 division protein ftsW.
BACILLUS cereus (strain ATCC 14579 / DSM 31).
Bacillus cereus (strain ATCC 14579 / Bacillus.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Msv052 (WSSV109).
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Viruses; dsDNA viruses, no RNA stage; Nimaviridae.
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88.9%; Pred. No. 1.5e+02;
iive 0; Mismatches 1;
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                                                               Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative (
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Best Local Similarity 88.5
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SEQUENCE FROM N.A.
                   SIGNAL
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"Identification of a nucleocapsid protein (VP35) gene of shrimp white spot syndrome virus and characterization of the motif important for targeting VP35 to the nuclei of transfected insect cells."; Virology 293:44-53(2002).
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Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
Lo C.F., Kou G.H.;
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Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
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"Pseudomonas aeruginosa PA14 pathogenicity island (PAPI) 1.";
"Pseudomonas aeruginosa PA14 pathogenicity island (PAPI) 1.";
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY273869; AAP84197.1; -.
Hypothetical protein.
SEQUENCE 78 AA; 8977 MW; 9B37EF21434C91A1 CRC64;
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Pred. No. 50;
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Lo C.-F., Kou G.-H.;

Submit-Led (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF332093; AAL33056.1; -.

EMBL; AF440570; AAL88977.1; -.
SEQUENCE FROM N.A.
Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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Search completed: March
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RESULT 15
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SEQUENCE FROM N.A.
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
Hypothetical protein.
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Dufreene d. a morile marine Synechococcus.";
Nature 424:1037-1042(2003).
EMBL; BX565693; CAE08151.1; -.
Hypothetical protein; Signal. Complete proteome.
1 22 Potential.
SIGNAL 1 22 Rotential.
SIGNAL 1 AA; 17551 MW; 12535EA&67CAC423B CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Created)

01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Hypothetical protein.

Hypothetical protein.

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
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80.0%; Score 32; DB 11; Length 102;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels
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80.0%; Score 32; DB 16; Length 17

Best Local Similarity 77.8%; Pred. No. 1.1e+02;

Matches 7; Conservative 1; Mismatches 1; Indels
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102 AA; 12058 MW; 9FCD4A6CA10276A7 CRC64;
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=84588;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
Hypothetical protein precursor.
SYNW1636.
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                                                                                                             PRT;
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SEQUENCE FROM N.A.
MEDLINE=22825697; PubMed=12917641;
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                              24 SLELPLOVL 32
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||||||| :| 7 SLLLPLLVL 15

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SEQUENCE FROM N.A.

STRAIN=CFSTBL/60; TISSUE=SKin;

STRAIN=CFSTBL/60; PubMed=1121951;

Kawai J., Shinadawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinadawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schifful I.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Bromstein M.J., Bult C., Fletcher C., Fullita M., Marion M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoco N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nyashiaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.;

"Functional ampotation of a full-length mouse cDNA collection.";
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                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoscomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
MCBI_TaxIb=10090;
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GO; GO:0003754; F:chaperone activity; IEA.
GO; GO:0005489; F:chaperone ransporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; PR001450; 4Fe45_ferredoxin.
PROSITE; PS00198; 4Fe45_FERREDOXIN; 4.
               01-JUN-2011 (TrEMBLrel. 17, Created)
01-JUN-2011 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
A030007E19R1k protein.
MUS MUNCHISRIK.
196 AA
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PRT;
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EMBL; AK020699; BAB32180.1; -.
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Best Local Similarity 66.7
Matches 6; Conservative
PRELIMINARY;
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145 ALLLPVQLL 153
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Sequence Sequence Sequence

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Patent No. 629434
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF ENERGY
TITLE OF INVENTION:
THE REFERENCE:
THE REFERENCE:
TOWNERN FILING DATE:
TOWNERN FILING DATE:
THE APPLICATION NUMBER:
THE OF SEQ ID NOS:

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| Sequence 80, Application US/09918243
| Sequence 80, Application US/09918243
| GENERAL INFORMATION, Timothy J.
| APPLICANT: Cannon, Martin J.
| APPLICANT: Santin, Alessandro
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
| TITLE OF INVENTION WHERE: US/09/918,243
| CURRENT FILING DATE: 2001-07-30
| PRIOR FILING DATE: 2001-07-30
| NUMBER OF SEQ ID NOS: 136
| SEQ ID NO 80
| LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               In 100.0%; Score 50; DB 3; Length 9; Similarity 100.0%; Pred. No. 3e+05; 9; Conservative 0; Mismatcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Residues 207-215 of the SCCE protein US-09-502-600-80
PCT-US94-07329-10
PCT-US94-07329-11
                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 9; Conserv
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     RESULT 2
US-09-918-243-80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                             March 1, 2004, 17:21:46; Search time 11.8889 Seconds (without alignments) 39.081 Million cell updates/sec
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Sequence 13,
Sequence 19,
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Sequence 2,
Sequence 2,
Sequence 3,
Sequence 3,
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Sequence 1
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/cgn2 = //prodata/2/iaa/5A_COMB.pep:*
/cgn2 = 6/prodata/2/iaa/5B_COMB.pep:*
/cgn2 = 6/prodata/2/iaa/6A_COMB.pep:*
/cgn2 = 6/prodata/2/iaa/6B_COMB.pep:*
/cgn2 = 6/prodata/2/iaa/POTUS_COMB.pep:*
/cgn2 = 6/prodata/2/iaa/POTUS_COMB.pep:*
                          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-679-279-15
US-09-679-279-13
US-08-472-228-19
US-08-146-831-19
US-08-06-946-10
US-08-096-946-10
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US-08-768-859A-16
US-08-768-859A-21
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US-08-057-146-12
US-09-154-344-12
US-09-644-600-4
US-09-654-600A-4
US-09-654-600A-4
US-08-824-84-2
US-08-824-84-2
US-08-930-188-2
US-08-930-188-2
US-08-330-188-2
US-08-330-188-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                                 M protein - protein search, using sw model
                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
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Match Length
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US-08-557-146-12
; Sequence 12, Application US/08557146
; Patent No. 5834290
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178 GPLVCRGTL 186
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STRANDEDNESS: sing
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                                                                                                       RESULT 4
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Sequence 33, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
APPLICANT: COLBITTS, TRACEY L.
APPLICANT: COLBITTS, TRACEY L.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STRONPB, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: NOVEL SERINE PROSTATE
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS: 76
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE
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Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                        100.0%; Score 50; DB 4; Length 9; 100.0%; Pred. No. 3e+05; cive 0; Mismatches 0; Indels
                                  NAME/KBY: CHAIN
OTHER INFORMATION: Residues 207-215 of the SCCE protein S-09-918-243.e0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: TELEGRAPHIC FEAT.

STATE: TELEGRAPHIC FORM:

CONTRY: USA

ZIP: 60064-350 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

COMPUTER: PastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/944,483

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6183.US.01
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ATTORNEY, AGENT INFORMATION:
NAME: BECKET, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
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SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 9; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GPLVCRGTL 9
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   FEATURE:
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Sequence 4, Application US/09027337B

Patent No. 5972616

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: Tacat and Ovarian Carcinomas
FILE REPERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B

CURRENT FILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 13
SEQ ID NO 4

LENGTH: 225
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ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to
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APPLICANT: Egelrud, Torbjorn
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: New York
CITY: New York
                                                                                                                                                                                                                                       CITY: New YOLK
STATE: New YORK
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER SEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: BOYON ALA:
ATTORNARY/ABGNT INFORMATION:
MAME: Steiner, Aichard J.
REDISTRATION NUMBER: 35,372
REPERBURGE/DOCKET NUMBER: 1103326-181
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
myor- amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 50; DB 2; Length 225; Best Local Similarity 100.0%; Pred. No. 0.14; Matches 9; Conservative 0; Mismatches 0; Indels
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Log 0; Indels
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Query Match
Best Local Similarity 100.
Matches 9; Conservative
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NUMBER OF SEQ ID NOS: 98
SEQ ID NO 4
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: SCCE US-09-654-600A-4
                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: SCCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 GPLVCRGTL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 GPLVCRGTL 187
                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GPLVCRGTL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GPLVCRGTL 9
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Bgelrud, Torbjorn
APPLICANT: Bgelrud, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Brzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
                                                                Score 50; DB 2; Length 225;
Pred. No. 0.14;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
21P: 10036-2737
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Datemin Release #1.0, Version #1.25 (EPO)
SOFTWARE: PATEMIN RELEASE #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
NAWE: Steiner, Richard J.
REGISTRATION NUMBER: 35,372
REGISTRATION NUMBER: 31,326-181
TELECHONE: (212) 354-8133
INPORMATION FOR SEG ID NO: 12: SEQUENCE GIRARATICS:
LENGTH 1225 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 50; DB 2; Length 225; 100.0%; Pred. No. 0.14; tive 0; Mismatches 0; Indels
; OTHER INFORMATION: similar domain in TADG-15 JS-09-027-337-4
                                                                                                                                                                                                                                                                   JS-09-154-344-12

Sequence 12, Application US/09154344

Patent No. 5981256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-09-644-600-4
Sequence 4, Application US/09644600
Patent No. 6451500
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
                                                                                                       ;
0
                                                                Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                 1 GPLVCRGTL 9
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Gaps
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Sequence 4, Application US/09654600A

Sequence 4, Application US/09654600A

Patent No. 6649741

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: TARG-15: An Extracellular Serine Protease

TITLE OF INVENTION: TOVERENCE: D6064CIP/D

FILE REFRENCE: D6064CIP/D

CURRENT PILING DATE: US/09/654,600A

CURRENT FILING DATE: 1999-10-20

PRIOR FILING DATE: 1999-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Beglind, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Bazyme (SCCE)
NUMBER OF SEQUENCES: 17
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease TITLE OF INVENTION: Overexpressed in Carcinomas FILE PREPRENCE: D6064CIP/D CURRENT APPLICATION NUMBER: US/09/644,600
CURRENT FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR APPLICATION NUMBER: 09/027,337
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: 09/027,337
NUMBER: OF SEQ ID NOS: 98
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 50; DB 4; Length 225; ilarity 100.0%; Pred. No. 0.14; Conservative 0; Mismatches 0; Indels
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us-09-905-083-80.rai

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Sequence 2, Application US/09154344 Patent No. 5981256
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REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION:
TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 14-21
       TELEFAX: 415-845-4166
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acids
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-09-154-344-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 GPLVCRGTL 215
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                                                                                                                                                                                                                              IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 532504
                                                                                                                                                                                                                                                                                                                                 US-08-824-874-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-154-344-2
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ADDA...
STREET: A..
CITY: New York
CUMTRY: New York
COUNTRY: U.S.A.
ZIP: 10.56-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATIOR SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424-1995
CLASSIFICATION NUMBER: 35,372
REGISTRATION NUMBER: 35,372
REGISTRATION NUMBER: 35,372
REGISTRATION NUMBER: 35,372
RELEPAN: (212) 819-8783
TTELEPAN: (212) 819-8783
TTELEPAN: (212) 819-8783
TTELEPAN: (212) 84-8113
INPORMATION FOR SEQ ID NO: 2:
"TQUBNCE CHARACTERISTICS:
"TH: 253 anino acids
"TIPORMATION CALON INFORMATION:
"TO: 10.00 2:
"TO: 10.00 
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100.0%; Score 50; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: BR ESTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08824874
Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKKEIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
CONTRY: USA
ZIP: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 GPLVCRGTL 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agtent No. 596120.
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hanson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
Score 50; DB 2; Length 253;
Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 100.0%; Score 50; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 0.16; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Recombinant Stratum Corneum Chymotrypt TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 1
NUMBER OF SEQUENCES: 1
NUMBER OF SEQUENCES: 1
NUMBER OF SEQUENCES: 1
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BA PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1955
CLASSIFICATION: ATTORNEY TO STATE TO ST
                                                                                                         0; Indels
                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 GPLVCRGTL 215
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US-09-210-084-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                               APPLICANT: Dixon, Eric P.
APPLICANT: Dixon, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMTIOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: 3
CORRESPONDENCE ADDRESS: 3
CORRESPONDENCE ADDRESS: CITL I Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis STREET: Indiana
COUNTRY: United States of America
ZIP: 46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 50; DB 3; Length 253; 100.0%; Pred. No. 0.16; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-210-084-3
US-09-210-084-3
; Sequence 3, Application US/09210084
; Patent No. 619751
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
PILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REPERENCE/DOCKET NUMBER: X9239
TELECHONE: 317-277-1090
TELEFRAX: 317-277-1090
                                         Sequence 2, Application US/08930188
Patent No. 6093397
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 GPLVCRGTL 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA
USA
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COUNTRY: US
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TY
JS-08-930-188-2
ESULT 12
S-08-930-188-2
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COMPUTER STANDALE FORE:

COMPUTER THE COMPATION COMPATIO
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INFORMATION FOR SEQ IN NO. 3:

SRUDNEE CHARACTERISTICS:
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Db 207 GPLVCRGTL 215
Search completed: March 1, 2004, 17:38:25
Job time : 11.8889 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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M protein - protein search, using sw model

: uo un

March 1, 2004, 17:16:55; Search time 45.5556 Seconds (without alignments) 55.820 Million cell updates/sec

US-09-905-083-80 50 itle:

1 GPLVCRGTL 9 erfect score: ednence: BLOSUM62 Gapop 10.0 , Gapext 0.5 coring table:

1586107 segs, 282547505 residues earched:

otal number of hits satisfying chosen parameters:

1586107

linimum DB seq length: 0 faximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Jatabase :

geneseqp1990s: geneseqp2000s:\* geneseqp2001s:\* geneseqp2003as:\* geneseqp2003as:\* A Geneseq 29Jan04:\*

Pred. No. is the number of regults predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

# SUMMARIES

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	lo B	Нишап	Human	Human	Human	Human	Human	Human	Нишал	Human	Human	Human	Human	Amino	Pro	Pro	Human	OVa	Human	Por	Nove]	Nove.	Nove	Нишап	9	Human
	Description	Aae08285	Ada05738	Ada05736	Ada05744	Aab98502	Ada05742	Ada05732	Ada05734	Aar67888	Aaw05383	Abb84421	Abb84406	Aau82740	Abu07440	Abu07471	Abr58471	Adb80484	Aab21326	Abb84420	Aau86677	Aau23217	Aau23752	Aau17043	Adb60011	Aab21298
SUMMAKIBS	ID	AAE08285	ADA05738	ADA05736	ADA05744	AAB98502	ADA05742	ADA05732	ADA05734	AAR67888	AAW05383	ABB84421	ABB84406	AAU82740	ABU07440	ABU07471	ABR58471	ADB80484	AAB21326	ABB84420	AAU86677	AAU23217	AAU23752	AAU17043	ADB60011	AAB21298
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di	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	94.0	90.0	0.06	90.0	0.06	90.0	90.0
	Score	50	20	50	20	50	20	20	20	20	20	50	20	20	50	20	50	50	50	47	45	45	45	45	45	4. 10
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	ABP64969 ABR55400 AAU16971	AAB21297 AAB21305 ABB84419 AAB21306	ABJ26666 ABG19361 ABB84409	AAB11/13 AAB66315 AAB82214 AAB82212 AAY48056	AAWS8064 AAWS8063 AAW11019 AAG75172 ADA50560
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## ALIGNMENTS

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Human stratum corneum chymotrypsin enzyme peptide #50 (residues 207-215)
                                                             Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.
           AAE08285 standard; peptide; 9 AA.
                                      (first entry)
                                      01-NOV-2001
                         AAE08285;
RESULT 1
       AAE0828
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Homo sapiens

WO200159158-A1.

16-AUG-2001.

07-FEB-2001; 2001WO-US003977.

11-FEB-2000; 2000US-00502600.

(UYAR-) UNIV ARKANSAS

O'brien IJ;

WPI; 2001-514676/56.

Diagnosing cancer comprises detecting stratum corneum chymotrypsin enzyme

Claim 25; Page 113; 127pp; English.

The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

Sequence 9 AA;

Query Match

Length 9; DB 4; 100.0%; Score 50;

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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DM, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkers RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
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                                                                                                                                                                                                                                                                                       human, NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachaxia; cancer; neurodegenerative disorder; Alahaimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
               Gaps
                   ö
                   Indels
100.0%; Pred. No. 1.4e+06; vative 0; Mismatches 0;
                                                                                                                                                                  ADA05738 standard; protein; 181 AA.
                                                                                                                                                                                                                                                              Human NOV18d protein SEQ ID NO:98.
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2002US-0381042P.
2002US-0381642P.
2002US-0383656P.
2002US-0383831P.
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                                                                                                                                                                                                                                 (first entry)
     Best Local Similarity 100.
Matches 9, Conservative
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                                                    1 GPLVCRGTL 9
                                                                                 GPLVCRGTL 9
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15-OCT-2001; 2
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22-OCT-2001)
24-OCT-2001)
24-OCT-2001)
29-OCT-2001)
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05-OCT-2001;
05-OCT-2001;
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                                                                                                                                                    A05738
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The present invention describes NoVX proteins, where X can be 1 to 55 cc (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit composition or more containers, the composition described above; (3) an isolated nucleic acid containers, the composition described above; (3) a call or more comprising the nucleic acid molecule described above; (5) a cell or comprising the nucleic acid molecule described above; (5) a cell or comprising the nucleic acid molecule described above; (5) a cell or presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above collypeptide or nucleic acid molecule in a first mammalian subject; (9) a collypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for above; (11) a method of aberrant physiological interactions of the polypeptide (11) a method of a pathology associated with the polypeptide; (12) a method for modulating or pathology associated with the polypeptide; (12) a method for modulating or pathology associated with the above polypeptide. NoVX or preventing a pathology associated with the above polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic correct or syndrome associated with a human disease. The polypeptide or the nucleic syndrome associated with a human disease. The polypeptide or the nucleic disease, immune disorders such as Alabeimer's disease or besity, infections, cancer, concerved because as the mucleic acid soles as a place of a pathology associated with a human disease. The polypeptide or probes, in chromosome mapping, ilssue typing, preventiv
                                                                                               New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.
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                                                                                                                                                                                                                                                                                                           Claim 1; Page 171; 586pp; English
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Best Local Similarity 100.
Matches 9; Conservative
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WPI; 2003-381626/36.
N-PSDB; ADA05737.
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09-0CT-2001, 20010S-0328044P.
09-0CT-2001, 20010S-0328044P.
12-0CT-2001, 20010S-0328844P.
15-0CT-2001, 20010S-0328844P.
17-0CT-2001, 20010S-0338844P.
18-0CT-2001, 20010S-033814P.
18-0CT-2001, 20010S-0339266P.
24-0CT-2001, 20010S-0343629P.
24-0CT-2001, 20010S-034386P.
25-0CT-2001, 20010S-034386P.
19-APR-2002, 2002US-0373817P.
16-MAY-2002, 2002US-0373817P.
                                                                                                                                                                                                                                                                       16-MAY-2002; 2002US-0381042P.
17-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0383656P.
29-MAY-2002; 2002US-038331P.
25-UUN-2002; 2002US-0391335P.
01-OCT-2002; 2002US-00262511.
                                                 02-OCT-2002; 2002WO-US031373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmacogenomics
               WO2003029424-A2
Homo sapiens
                                 10-APR-2003
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ott T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or

Claim 1; Page 170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a cell
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
disease associated with altered levels of expression of the above
polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
use in treating a pathology that is related to an aberrant expression or

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aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide; no amend; and (14) a method for producing the above polypeptide; now a sequences have antidiabetic, anoredtic, antibacterial, virucide, now; immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian antilippement activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic collosocials and be used to diagnose, treat or prevent metabolic collosocials acides and various disorders such as Alzheimer's disease or Parkinson's disorders from the nucleic acids can also used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and proportion the present sequence represents a human NOVX from the
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09-0CT-2001, 2001US-032791,7P.
09-0CT-2001, 2001US-0328059P.
09-0CT-2001, 2001US-0328056P.
12-0CT-2001, 2001US-0328449P.
15-0CT-2001, 2001US-0328444P.
15-0CT-2001, 2001US-0339444P.
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2001US-032743PP.
2001US-032741PP.
2001US-0327917P.
2001US-0328029P.
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24-OCT-2001; 2001US-0339266P.
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29-OCT-2001; 2001US-0349575P.
01-NOV-2001; 2001US-0346357P.
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Best Local Similarity luv.
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05-OCT-2001;
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The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising in one or more containers, the composition described above; (3) an isolated nucleic acid molecule described above; (3) an isolated nucleic acid molecule described above; (3) an isolated nucleic acid molecule described above; (5) a cell or comprising the nucleic acid molecule described above; (5) a cell or binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying an agent that binds to the polypeptide described above; (10) a method for identifying a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of activity or of latency or predisposition to a berrant physiological interactions of the polypeptide; (12) a method for modulator of activity or of latency or predisposition to the activity of the polypeptide described above; (13) methods of treating the activity of the polypeptide described above; (13) methods of activities, and antilipaemic activities, and can be used in gene therapy. The mammal; and (14) a method for producing the above polypeptide is useful in manufacturing a medicament for treating a pathology associated with a human disease. The polypeptide or the nucleic significance and to disables or prevent metabolic activities, and can be used in gene therapy. The solutions and be used to disables or prevent metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerbusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 172; 586pp; English.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373826P.
19-APR-2002; 2002US-0373844P.
25-APR-2002; 2002US-03193844P.
16-MAY-2002; 2002US-0381037P.
16-MAY-2002; 2002US-0381038P.
17-MAY-2002; 2002US-0381642P.
17-MAY-2002; 2002US-0381642P.
17-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0383811P.
25-JUN-2002; 2002US-03938381P.
25-JUN-2002; 2002US-03938381P.
25-JUN-2002; 2002US-03938381P.
                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2003-381626/36.
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present invention.

neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the

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                                                    Gaps
                                                    ö
Query Match 100.0%; Score 50; DB 6; Length 224; Best Local Similarity 100.0%; Pred. No. 1.6; Matches 9; Conservative 0; Mismatches 0; Indels
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Human NOV18f protein SEQ ID NO:102.

(first entry)

06-NOV-2003

ADA05742;

The present invention relates to human tumour antigen-derived gene 15 (TADG-15) protein and coding sequence (see AAH23601 and AAB99500). TADG-15 is an extracellular serine protease. It was found that TADG-15 is over-expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20 residues that lack TADG-15 protein or its fragments of 9-20 residues that lack TADG-15 protein or its fragments of 9-20 getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic or therapeutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TADG-15 Novel extracellular serine protease, termed tumor antigen-derived gene 15 protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast, ovarian cancer. 0, Gaps Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain. Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer; 100.0%; Score 50; DB 4; Length 225; 100.0%; Pred. No. 1.6; 0; Indels cive 0; Mismatches 0; Indels tumour antigen-derived gene 15; serine protease; Stratum Corneum Chymotryptic Enzyme; SCCE. AAB98502 standard; protein; 225 AA ADA05742 standard; protein; 247 AA. Example 10; Fig 1; 130pp; English. 99US-00421213. 20-OCT-2000; 2000WO-US029095. (first entry) 9; Conservative Tanimoto H; 193 GPLVCRGTL 201 179 GPLVČRGTL 187 (UYAR-) UNIV ARKANSAS. 1 GPLVCRGTL 9 WPI; 2001-381031/40. 1 GPLVCRGTL Similarity Sequence 225 AA; WO200129056-A1. Homo sapiens. 20-OCT-1999; O'brien TJ, 03-AUG-2001 26-APR-2001. Query Match Best Local 9 Matches RESULT 6 ADA05742 AAB98502 a a ઠે ò

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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CBA, Shenoy SG;
Shimkets RA, Rochenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK; human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia. 200105-03280299 200105-0328044P. 200105-0328056P. 200105-0328499P. 200105-0329414P. 2001US-0330309P.
2001US-0341058P.
2001US-034956EP.
2001US-0349575P.
2002US-0349575P.
2002US-0349577P.
2002US-0373817P.
2002US-0373814P.
2002US-0373814P.
2002US-0373814P.
2002US-0373814P.
2002US-0373814P.
2002US-0373814P.
2002US-0381034P.
2002US-0381034P.
2002US-0381034P.
2002US-0381034P.
2002US-0381034P. 02-OCT-2002; 2002WO-US031373 (CURA-) CURAGEN CORP. WPI; 2003-381626/36. N-PSDB; ADA05741 19-APR-2002; 19-APR-2002; 19-APR-2002; 22-APR-2002; 16-MAY-2002; 16-MAY-2002; 09-OCT-2001; 09-OCT-2001; 09-OCT-2001; 01-NOV-2001; 17-APR-2002; Homo sapiens Shimkets RA, Eisen AJ, G 09-OCT-2001; 16-MAY-2002; 28-MAY-2002; 10-APR-2003 

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; Page 172; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the

presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide described above constraint physiological interactions of the polypeptide; (11) a method of a pathology associated with the polypeptide; (12) a method for modulating or pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a mammal; and (14) a method for producing the above polypeptide; NoVX sequences have antidabetic, anometric, antibacterial, virucide, immunomodulator, cytostatic, noctropic, neuroprotective, antipaxinsonian and antilipaemic activities, and can be used in gene therapy. The collision activities, and can be used in gene therapy. The solls is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders such as Alzheimer's disease or Parkinson's dispense, immune disorders such a shadenes and various probes, in ohromosome mapping, tissue typing, preventive medicine and present invention. 0; human, NOVX, antidiabetic, anorectic, antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabeter; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia. Gaps . 0 1000.0%; Score 50; DB 6; Length 247; 1000.0%; Pred. No. 1.8; 0; Indels 0; Mismatches ADA05732 standard; protein; 250 AA. Human NOV18a protein SEQ ID NO:92. 2001US-0327435P. 2001US-0327449P. 2001US-0327917P. 2001US-0328849P. 2001US-0329414P. 2001US-0330142P. 2001US-0328029P 2001US-0328044P 02-OCT-2002; 2002WO-US031373 (first entry) 9; Conservative 193 GPLVČŘGŤĽ 201 1 GPLVCRGTL 9 Query Match Best Local Similarity present invention. Sequence 247 AA; WO2003029424-A2. 12-OCT-2001; 15-OCT-2001; 17-OCT-2001; 09-OCT-2001; 09-OCT-2001; 09-OCT-2001; Homo sapiens. 02-OCT-2001; 05-OCT-2001; 05-OCT-2001; 09-OCT-2001; 06-NOV-2003 10-APR-2003, ADA05732; Matches RESULT 7 ADA05732 a ð

present invention Sequence 250 AA;

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2001US-0341058P
2001US-034266P
2001US-0349575P
2001US-0346357P
2002US-0346357P
2002US-0346357P
2002US-0373817P
2002US-0373817P
2002US-0373817P
2002US-0373817P
2002US-0373817P
2002US-0373817P
2002US-0373817P
2002US-0373817P
2002US-0381038P
2002US-0381038P
2002US-0381038P
2002US-0381038P
2002US-0381038P
2002US-0381038P
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                                                                                                                                     (CURA-) CURAGEN CORP.
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N-PSDB; ADA05731.
                                                                                                                                                                                                                                    pharmacogenomics.
                                                                                                                                                 Smithson G, M
Patturajan M,
                       29-0CT-2001)
11-NOV-2001)
11-APR-2002)
119-APR-2002)
119-APR-2002
129-APR-2002
29-APR-2002
                                                                                                                                                                   Ji w, Miller
Shimkets RA,
Eisen AJ, Gal
                                                                                                                        01-OCT-2002;
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thson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, turajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM, T, Gorman L, Zerhueen BD, Anderson DW, Zhong M, Catterton E, W, Miller CE, Rastelli L, Stone DJ, Pena CBA, Shenoy SG; mkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; en AJ, Gangolli BA, Rieger DK, Spaderna SK;

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or

Claim 1; Page 169-170; 586pp; English

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described above and a carriar; (2) a kit composition comprising a polypeptide described above and a carribed; in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (6) a cell comprising the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample. (8) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapetuic agent for method of identifying a pathology that is related to an aberrant expression or betweening for a modulator of activity or of latency or prespection or aberrant physiological interactions of the polypeptide; (11) a method of coreceiving for a modulator of activity or of latency or prespective in a pathology associated with the polypeptide; (12) a method for modulator of a pathology associated with the above polypeptide in a method for protective, antiparkinsonian antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a method coreceive, antiparkinsonian antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a method of sorderia, and can be used of disease such as diabetes or obesity, infections, cancering and pathology associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disease, immune diseated with a human disease. The polypeptide or the nucleic acids can also be used as obseity, infections, cancer and antilipaemic activities, and an above

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                                                                                                                                                                                                            human, NOVX, antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipatkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obseity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                        Gaps
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A, Edinger SR, Ellerman K, Malyankar UM;
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0
 100.0%; Score 50; DB 6; Length 250; 100.0%; Pred. No. 1.8;
                        0; Indels
                       0; Mismatches
                                                                                                                        ADA05734 standard; protein; 252 AA
                                                                                                                                                                                          Human NOV18b protein SEQ ID NO:94.
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2002US-0373826P.
2002US-0373884P.
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2001US-0327449P.
2001US-0327917P.
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2001US-0329414P.
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                                                                                                                                                                                                                                                                                                                                                                                                                               09-OCT-2001; 2001US-0328029P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001US-0346357P
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                                                                                                                                                                   06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smithson G, Millet I, Pe
Patturajan M, Spytek KA,
Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                 204 GPLVCRGTL 212
                                             1 GPLVCRGTL 9
                                                                                                                                                                                                                                                                                                                WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                       09-0CT-2001, 2
12-0CT-2001, 2
15-0CT-2001, 2
17-0CT-2001, 2
16-0CT-2001, 2
18-0CT-2001, 2
                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                               ADA05734;
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Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Miller CE, Rastelli L, Stone DD, Pena CEA, Shenoy SG;
its RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
AJ, Gangolli EA, Rieger DK, Spaderna SK;
Ort T, Gorma
Ji W, Miller
Shimkets RA,
                                                                                      Eisen AJ,
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WPI; 2003-381626/36 N-PSDB; ADA05733

obesity, New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing pharmacogenomics.

Claim 1; Page 170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described and a carrier; (2) at the composition comprising a polypeptide described above and a carrier; (2) at the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell of comprising the nucleic acid molecule described above; (5) a cell of physpetide described above; (5) a cell of presence or amount of the above polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above adisease associated with altered levels of expression of the above; (10) a method for identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for method of identifying a pathology that is related to an aberrant expression of aberrant physiological interactions of the polypeptide; (11) a method of succession of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulation or a pathology associated with the above polypeptide in a method for producing the above polypeptide in a method for producing the above polypeptide in a method for producing the above polypeptide or the nucleic and antilipaemic activities, and can be used in gene therapy. The nucleic syndrome associated with a human disease. The polypeptide or the nucleic syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic syndrome associated with a human disease. The polypeptide or parking and disease or obesity, inchanced and parking in a pathology is a latency of issue or prevent we adjabetes or obesity in chromosome mapping, issue typing, preventive medicine and polypeptide and issued as an also be used as hybridiation present invention  $rac{1}{2}$ 

Sequence 252 AA;

Gaps ö 100.0%; Score 50; DB 6; Length 252; 100.0%; Pred. No. 1.8; cive 0; Mismatches 0; Indels Best Local Similarity 100. Query Match

Amyloid precursor protein protease; Alzheimer's disease; diagnosis;

Homo sapiens WO9631122-A1

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Human amyloid precursor protein protease.

31-DEC-1996 (first entry)

AAW05383 standard; protein; 253 AA

ð В RESULT 9 \*\*\*\*\*

AAR67888 standard; protein; 253 AA AAR67888; Human stratum corneum chymotrophic recombinant enzyme (SCCE).

(revised)
(first entry)

25-MAR-2003 09-AUG-1995

Little SP;

Dixon EP, Johnstone EM, (ELIL ) LILLY & CO ELI.

WPI; 1996-464694/46.

96WO-US004294.

02-APR-1996; 04-APR-1995;

10-OCT-1996.

Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis;

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The enzyme encoded by this sequence is used in pharmaceutical, cosmetic and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkratchic conditions (e.g. callosities or keratosis planis), ichthyoses, psociasis, eczema, etc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid pS507. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                              Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of specific inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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callosities; keratosis pilaris; ichthyoses; eczema.
                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 97; 137pp; English.
                                                                                                                   94WO-IB000166.
                                                                                                                                               93DK-00000725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                               (SYMB-) SYMBICOM AB
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les 9; Conserv
                                                                                                                                                                                                                                                           N-PSDB; AAQ81203.
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                             Homo sapiens.
                                                                                                                   20-JUN-1994;
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                                                                                       05-JAN-1995.
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N-PSDB; AAT39783

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New isolated human amyloid precursor protein protease - used to develop prods. for the treatment or diagnosis of associated conditions, esp. Alzheimer's disease.
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Claim 1; Page 44-45; 55pp; English.

Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAM39783) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. E. coli) or enkaryotic and testing of cods. useful for treating or develop products for the design and testing of cods. useful for treating or preventing conditions associated with beta-amyloid peptide, esp. Alzheimer's disease

Sequence 253 AA;

Gaps ö 100.0%; Score 50; DB 2; Length 253; 100.0%; Pred. No. 1.8; ive 0; Mismatches 0; Indels Ouery Match Best Local Similarity 100. Matches 9; Conservative

. 0

207 GPLVCRGTL 215 φ GPLVCRGTL Н

ESULT 11

ABB84421 standard; peptide; 253 AA

08-NOV-2002. ABB84421;

Human SCCE protein N-terminal fragment SEQ ID 48.

(first entry)

SCCE, human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.

Homo sapiens

WO200262135-A2

15-AUG-2002.

08-FEB-2002; 2002WO-IB001300

09-FBB-2001; 2001CA-02332655. 09-FBB-2001; 2001DK-00000218.

(EGEL/) EGELRUD T. (HANS/) HANSSON L.

Egelrud T, Hansson L;

WPI; 2002-643380/69.

Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.

Example 6; Page 37; 74pp; English.

**\$\$#\$\$\$**\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$

This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous scce or its variant in skin. The product of the invention is useful as a model.

CC or ameliorate a pathogenic condition, for development or testing of a comment or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for skin disease or component or tengosticin effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an compound or composition effective for the prevention or treatment of an inflammatory skin diseases selected from diseases consisting of epidermal inflammatory skin diseases selected from diseases consisting of epidermal inflammatory subject at the invention or treatment of an example of prutitus, atopic dermatitis, eczema, acne and inherited skin diseases or with epidermal hyperkeratosis. The mammal of the invention is also useful or potential compounds and compositions for relieve of various skin diseases consisting of contrain compounds and compositions for relieve of various skin diseases of tragment of the human stratum corneum chymotryptic enzyme, SCCE transgenic mammals described in the invention

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Sequence 253 AA;

; 0 Gaps ö 100.0%; Score 50; DB 5; Length 253; 100.0%; Pred. No. 1.8; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.

207 GPLVCRGTL 215 Q 1 GPLVCRGTL ઠે 셤

RESULT 12 ABB84406

ABB84406 standard; protein; 253 AA.

ABB84406;

08-NOV-2002 (first entry)

Human SCCE protein.

SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protesse; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme. 

WO200262135-A2

15-AUG-2002

08-FEB-2002; 2002WO-IB001300.

09-FEB-2001; 2001CA-02332655. 09-FEB-2001; 2001DK-00000218.

EGELRUD T. HANSSON L. (EGEL/) I ä Egelrud T, Hansson

WPI; 2002-643380/69.

N-PSDB; ABQ76226

Transgenic mammal or its embryo useful as model for human disease, has hererologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.

Claim 10; Page 58-59; 74pp; English.

This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence

coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologues acce or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin oacter. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an acceptance of inflammation, dermal inflammation, pruritus, atopic dermatities, eczema, ance and inherited skin diseases with epidermal hyperkeratosis. The mammal of the invention is also useful as a model for the prevention of compounds and compositions for relieve of various skin diseases where itch is a component. This sequence represents the human stratum chymotryptic anzyme, SCCE which is a serine procease synonymous with human kallikrein 7 (KLK7) and is used in the development of the

Sequence 253 AA;

0; Gaps 100.0%; Score 50; DB 5; Length 253; 100.0%; Pred. No. 1.8; 0; Indels tive 0; Mismatches 0; Indels 9; Conservative Ouery Match Best Local Similarity Matches 9; Conserv

1 GPLVCRGTL 9

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207 GPLVCRGTL 215

ESULT 13 AU82740

AAU82740 standard; protein; 253 AA. AAU82740;

23-APR-2002 (first entry)

Amino acid sequence of novel human protease #39.

Human, protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mocd disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.

WO200200860-A2.

03-JAN-2002.

26-JUN-2001; 2001WO-US020171

26-JUN-2000; 2000US-0214047P

(SUGE-) SUGEN INC.

Sudarsanam S, Manning G, Caenepeel S; Whyte D, Charydczak G; Plowman G,

WPI; 2002-139913/18. N-PSDB; ABK31782

Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory disorders 

The present invention relates to the isolation of novel human proteases, and the mucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma) cardiovascular diseases (e.g. inflammatory diseases and asthma) cardiovascular diseases (e.g. inflammatory coronary thrombosis) brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. theumator) attributes and psoriasis), central or peripheral nervous system diseases, migraines, pain, sexual dysfunction, mood disorders attention disorders, hypotension, hypertension, psychotic disorders, cognition disorders (e.g. Alzhaimer's disease, Parkinson's disease) and dyskinesias. The mucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency disucement and macular degeneration. AAU82702-AAU82760 represent the novel human proteases of the invention Claim 6; Fig 2N; 313pp; English. 

Sequence 253 AA;

Gaps ö 100.0%; Score 50; DB 5; Length 253; 100.0%; Pred. No. 1.8; 0; Indels 0; Mismatches Local Similarity 100. Query Match Matches

207 GPLVCRGTL 215 σ 1 GPLVCRGTL a ઠ

RESULT 14 ABU07440 ABU07440 standard; protein; 253 AA. ABU07440;

(first entry) 28-JAN-2003

Protein differentially regulated in prostate cancer #43:

Prostate cancer, gene expression, differential regulation, molecular marker, drug target, cancer detection, cancer diagnosis; cancer staging; cancer grading, cancer assessing;

WO200281638-A2.

17-OCT-2002.

08-APR-2002; 2002WO-US010824. 

06-APR-2001; 2001US-0281731P. 06-APR-2001; 2001US-0281732P.

(ORIG-) ORIGENE TECHNOLOGIES INC.

Jay G; Sun Z, WPI; 2003-058520/05. N-PSDB; ABX10343 Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

Claim 1; Page 293-294; 416pp; English.

The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially regulated in the sample, where the number is indicative of the probability that the sample comprises

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prosecte cancer. It, it useful for assessing a cherapture of preventive intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Preferably, the expression levels of at least 10 genes are determined.

(I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. It is useful as molecular markers, as drug targets, and for detecting, is useful as molecular markers, as drug targets, and for detecting, products are used activity of the polypeptide, and dagnosing, straging, grading, assessing, monitoring, prognesticating, products are used in the diagnostic test to assay for presence of cancer e.g., in tissue sections in biopsy sample, in total RNA, in lymph, in blood etc. (I) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. The polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus for searching specific binding partners of the polypeptide and thus of specific genes, and groups of genes, expressed in pathways to physiologically relevant to prostate cancer. The identification of functional and disease pathways and the delineation of targets in these pathways which are useful in diagnostic, therapeutic, and clinically relevant to prostate cancer penalts, and clinically and become of a protein disease pathways and the delineation of targets in these pathways which are useful in diagnostic, therapeutic, and clinically and proved and the delineations of argetic applications.
preventive
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100.0%; Score 50; DB 6; Length 253; 100.0%; Pred. No. 1.8;
                                                                   0; Indels
                                                                   Mismatches
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                                  Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
Sequence 253 AA;
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Gaps

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207 GPLVCRGTL 215 σ 1 GPLVCRGTL

ABU07471 standard; protein; 253 AA. (first entry) 28-JAN-2003 ABU07471;

Protein differentially regulated in prostate cancer #74.

Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer monitoring

Homo sapiens.

WO200281638-A2

17-OCT-2002.

08-APR-2002; 2002WO-US010824.

06-APR-2001; 2001US-0281731P. 06-APR-2001; 2001US-0281732P.

(ORIG-) ORIGENE TECHNOLOGIES INC

Jay G; Sun Z, WPI; 2003-058520/05. N-PSDB; ABX10375.

the number is indicative of the probability that the sample comprises prostate cancer. (1) is useful for assessing a therapeutic or preventive intervention in a subject having a profette cancer, which involves determining the expression levels in a sample comprising profetate tissue of target genes which are differentially-regulated in prostate cancer. Or fearaget genes which are differentially-regulated in prostate cancer. The fearably, the expression levels of at least 10 genes are determined. (1) is also useful for identifying agents that modulate a biological. (2) excivity of a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to medulate a biological activity of the polypeptide, and the test agent markers and conditions effective or determining whether the test agent modulates the biological activity. (1) is useful as molecular markers, as drug targets, and for detecting, conditions especially relating to prostate cancer. (1) and its expression conditions especially relating to prostate cancer. (1) and its expression conditions especially relating to prostate cancer. (1) and its expression conditions especially relating to prostate cancer. (1) and its expression of cancer, its stage of development, the nature of genetic defect, or earthing specific binding partners of the polypeptide encoded by (1) can be used as target for therapy or drug discovery. (1) can also be used for expressing the polypeptide encoded by (1) can be used as target for therapy or drug discovery. (1) can also be used for expressing the polypeptide and thus discovery. (1) can also be used for expressing the polypeptide and thus continued and disease pathways and the delineation of targets in these applications to treat prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways which are useful in disease pathways and the delineation of appropriate cancer. The identification of applications. This is the amino acid sequence The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises Novel genes which are differentially regulated in prostate cancer, usef for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients. Claim 1, Page 351; 416pp; English. regulated in prostate cancer 똩뿉뿉荚찞쳧읁윱윱윱윱윱윱윱윱윱윱윱윱윱윱윱윱윱윱윱윱윱윱윱윱윱윱

Sequence 253 AA;

Gaps . 0 100.0%; Score 50; DB 6; Length 253; 100.0%; Pred. No. 1.8; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 9; Conservative

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Sequence 90, Appl
Sequence 498, Appl
Sequence 488, Appl
Sequence 284, Appl
Sequence 742, App
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Sequence 69, Appl
Sequence 212, App
Sequence 68, Appl
Sequence 67, Appl
Sequence 5, Appli
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Sequence 80, Appl
Sequence 98, Appl
Sequence 3, Appli
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-905-081-80
US-09-906-1613-80
US-09-764-762-3
1 US-10-254-283-90
5 US-10-173-99-48
US-09-764-898-284
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US-09-764-898-284
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US-10-052-15694-69
US-10-055-5694-69
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Maximum Match 100*
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Sequence 12, Appl. Sequence 12, Appl. Sequence 1, Appl. Sequence 3, Appl. Sequence 5, Appl. Sequence 6, Appl. Sequence 10, Appl. Sequence 10, Appl. Sequence 11, Appl. Sequence 14, Appl. Sequence 14, Appl. Sequence 16, Appl. Sequence 16, Appl. Sequence 16, Appl. Sequence 17, Appl. Sequence 18, Appl.	Sequence 11, Appl Sequence 947, App Sequence 947, App Sequence 46, Appl
100-115-479-100-115-479-100-115-479-100-128-9-66-100-128-9-66-100-128-9-66-100-128-9-66-100-128-9-9-66-100-128-9-9-66-100-128-9-9-66-100-128-9-9-66-100-128-9-9-66-100-128-9-9-68-100-128-9-9-9-9-9-9-9-9-9-9-9-9-9-9-9-9-9-9-9	US-10-298-965-11 US-09-822-827-947 US-09-895-793-947 US-09-796-294-46
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## ALIGNMENTS

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USECULT INCREMENTATION: Sequence 80, Application US/09918243

GENERAL INFORMATION: Mattin J.

APPLICANT: Cannon, Mattin J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer

CURRENT FILING DATE: 2001-07-30

FRIOR PREPARATION NUMBER: US

NUMBER OF SEQ ID NOS: 136

INVERTY FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

INVERTY PRIME

FRATURE:

NAME/KEY: CHAIN

O'THER INFORMATION: Residues 207-215 of the SCCE protein

US-09-918-243-80

Query Match

Best Local Similarity 100.0%; Score 50; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.2e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

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I GPLVCRGTL 9

I GPLVCRGTL 9
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US-09-905-083-80
; Sequence 80, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:

us-09-905-083-80.rapb

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CITY: Palo Alto
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APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: O'Arian Cancer
TITLE OF INVENTION: O'Arian Cancer
FILE REPRENCE: D6223CIP/C/Div
CURRENT APPLICATION NUMBER: US/09/905,083
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 09/502,600
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 136
FEATURE OF SEQ ID NOS: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gabs
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                                                                                                                                                                                                                                                                                                                            NAME/KEY: CHAIN
OTHER INFORMATION: Residues 207-215 of the SCCE protein
3-09-905-083-80
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TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE Pharmaceuticals, Inc.
STREET: 3174 POTICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CHARVEEL, SEAN
APPLICANT: CHARVEEL, SEAN
APPLICANT: CHARVEEL, SEAN
APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: 05/214,047
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 98, Application US/09888615
Patent No. US20020064856A1
GENERAL INFORMATION:
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JS-09-764-762-3
S-09-764-762-3
Sequence 3, Application US/09764762
; Patent No. US20020068341A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
IS-09-8888-615-98
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Sequence 90, Application US/10264283
Sequence 90, Application US/10264283
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.590
CURRENT APPLICATION NOWBER: US/10/264,283
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 111
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 90
LENGTH: 253
TYPER: RAT
TYPER: RAT
CORRANISM: Homo sapiens
US-10-264-283-90
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Best Local Similarity 100.0%; Score 50; DB 14; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels (
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESD for Windows Version 2.0
SUFFWARE: FASTESD for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFCATION: *UNKnown>
PRIOR APPLICATION NUMBER: 09/210,084
FILING DATE: *UNKnown>
ATTONBY/AGBNT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-855-055
TELEPAX: 415-855-055
TELEPAX: 415-855-055
TELEPAX: 415-855-055
TELEPAX: 415-855-055
TELEPAX: 415-854-4166
INFORMATION OF SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
LINGTH: 253 amino acids
TYPP: amino acids
TYPP: amino acids
TYPP: amino acids
TYPP: TINGAT
TOPOLOGY: linear
TOPOLOGY: linear
TANDALATER SOURCE:
TANDALATER SOURCE:
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (148)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
1 LOCATION: (201)
2 CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (145)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (185)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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100.0%; Score 50; DB 15; Length 253;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 284, Application US/09764898
Patent No. US20020090673A1
GENERAL INFORMATION:
APPLICAMT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PJZ01
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 311
SOFTWARE: Patentin Ver. 2.0
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                PRIOR APPLICATION NUMBER: US 60/315,287
PRIOR PLING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR PRIOR PLES: 2001-04-12
NUMBER OF SEQ ID NOS: 163
SEQ ID NO 48
LENGTH: 253
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PRICE FILING DATE: 2001-06-18
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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US-09-764-898-284
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LENGTH: 247
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids 5-09-764-847-742
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LOCATION: (147)
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LOCATION: (201)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
JS-10-092-154-742
                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids MYMB/KEY: SITE 1000 NATURE AND ACCURATION: (142)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (148)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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S-10-092-154-742.
S-10-092-154-742.
Sequence 742, Application US/10092154
Publication No. US20330054375A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT APPLICATION DAIE: 2002-03-07
NUMBER OF ESQ 1D MOS: 2003
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 742
LENGTH: 247
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
FILENGE OF SEQ. ID NOS: 2003
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 742
LENGTH: 247
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90.0%; Score 45; DB 9; Length 247;
Best Local Similarity 88.9%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 1; Indels
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LOCATION: (145)
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LOCATION: (148)
                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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LOCATION: (145)
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APPLICANT: Taughder Jr., Raymonf J
APPLICANT: Anderson, David W
TITLE OF INVENTION: Not US20040024161Alel Human Proteins, Polynucleotides Encoding The
TITLE OF INVENTION: Nethods of Using the Same
FILE REPERENCE: 21402-191
FILE REPERENCE: 21402-191
CURRENT APPLICATION WUMBER: 60/243,642
PRIOR FILING DATE: 2000-10-26
PRIOR FILING DATE: 2000-10-26
PRIOR FILING DATE: 2000-10-26
PRIOR FILING DATE: 2000-10-26
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-31
PRIOR PRIOR APPLICATION WUMBER: 60/244,443
PRIOR FILING DATE: 2000-10-31
PRIOR FILING DATE: 2000-10-31
PRIOR FILING DATE: 2000-11-01
PRIOR PRIOR APPLICATION WUMBER: 60/244,493
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION WUMBER: 60/245,395
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2000-11-01
PRIOR PRIOR APPLICATION WUMBER: 60/245,315
PRIOR FILING DATE: 2000-11-02
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE
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NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 69
LENGTH: 250
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Query Match 90.0%; Score 45; DB 14; Length 247; Best Local Similarity 88.9%; Pred. No. 3.9; Matches 8; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 69, Application US/10055569A Publication No. US20040024181A1 GENERAL INFORMATION:
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Padigaru, Muralidhara
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Spytek, Kimberly A
Gilbert, Jennifer
Casman, Stacie
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Gerlach, Valerie L
Bdinger, Shlomit
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Gunther, Brik
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Stone, David
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Li, Li
Vernet, Corine
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Best Local Similarity 88.9<sup>5</sup>
Matches 8, Conservative
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CRGANISM: Homo sapiens
US-10-055-569A-69
                                                                                                                                                1 GPLVCRGTL 9
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US-10-055-569A-69
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UG-10-055-563-67

Sequence 67, Application UG/1005569A

PUblication No. UGS0040024181A

SEREIGLANT Gangoli, Esha A

APPLICANT Gangoli, Esha A

APPLICANT Galbert, Jennifer

APPLICANT Glanat, Stacie

APPLICANT Glibert, Jennifer

APPLICANT Glibert, Jennifer

APPLICANT Glibert, Jennifer

APPLICANT Mishau S

APPLICANT MINBER: G0/243 642

APPLICANT MINBER: G0/243 642

APPLICANT MINBER: G0/243 681

PRIOR PRIOR APPLICANTON NUMBER: G0/243 681

PRIOR PRIOR PRIOR DATE: 2000-10-27

PRIOR PRIOR APPLICANTON NUMBER: G0/243 681

PRIOR PRIOR PRIOR DATE: C000-10-31
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-27
PRIOR PELING DATE: 2000-10-31
PRIOR PELING DATE: 2000-11-31
PRIOR PILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/245,293
PRIOR PILING DATE: 2000-11-02
PRIOR PELING DATE: 2000-11-02
PRIOR PILING DATE: 2001-11-02
PRIOR PILING DATE: 200-11-02
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Best Local Similarity 77.8
Matches 7; Conservative
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APPLICANT: Millet, Isabelle
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Ellerman, Karen
APPLICANT: Ellerman, Karen
APPLICANT: Taupier Jr., Raymond J
APPLICANT: Taupier Jr., Raymond J
APPLICANT: Anderson, David B
APPLICANT: Anderson B
APPLICANT: Applicant B
APPLICANT: B
APP
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Patent No. US20020090673A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PZ01 UNMBER: US/09/764,898
CURRENT APPLICATION UNMBER: US/09/764,898
CURRENT APPLICATION DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 311
SOFTWARE PATENTIN Ver. 2.0
SEQ ID NO 212
LENGTH: 251
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CURRENT APPLICATION NUMBER: US/10/055,569A
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 60/243,642
PRIOR APPLICATION NUMBER: 60/243,320
PRIOR APPLICATION NUMBER: 60/243,320
PRIOR PRILING DATE: 2000-10-26
PRIOR PRILING DATE: 2000-10-26
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Publication No. US20040024181A1
BENERAL INFORMATION:
APPLICANT: Gangolli, Esha A
APPLICANT: Spytek, Kimberly A
APPLICANT: Glibert, Jennifer
APPLICANT: Glibert, Jennifer
APPLICANT: Blalock, Angela
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Gerlach, Valerie L
Edinger, Shlomit
Malyanker, Uriel
Stone, David
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Vernet, Corine
Shenoy, Suresh
Mishra, Vishnu S
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S-09-764-898-212
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                                  1 GPLVCRGTL 9
                                                                                                                                                                                                                                                                  SSULT 12
S-09-764-898-212
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S-10-055-569A-68
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us-09-905-083-80.rapb

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Segrence 5, Application US/09860739
Publication No. US20030166036A1
GENERAL INFORMATION:
Publication No. US20030166036A1
GENERAL INFORMATION:
APPLICANT: Hybritech Incorporated
APPLICANT: Hybritech Incorporated
APPLICANT: Riteenhouse, Harry
ITILE OF INVENTION: A Porcease and an Aminopeptidase Associated with Development of E
TITLE OF INVENTION: Protease and Aminopeptidase Associated with Development of E
TITLE OF INVENTION: Protease and Aminopeptidase Associated with Development of E
TITLE OF INVENTION: Protease and Aminopeptidase Associated with Development of E
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TITLE OF INVENTION: Protease and Aminopeptidase Associated with Development of E
TITLE OF INVENTION: Protease and Aminopeptidase Associated with Development of E
TITLE OF INVENTION: A POSTATE: US/09/860,739
CURRENT FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 5
SEQ ID NO S: SEQ ID NOS: SEQ ID NO SEQ ID 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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PRIOR APPLICATION NUMBER: 60/245,029
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/244,995
PRIOR PILING DATE: 2000-11-01
PRIOR PILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 60/245,293
PRIOR FILING DATE: 2000-11-02
PRIOR PILING DATE: 2000-11-02
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PALENTIN Ver. 2.1
LENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 82.0%; Score 41; DB 16; Length 276; Best Local Similarity 77.8%; Pred. No. 22; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

80.0%; Score 40; DB 10; Length 54;
Best Local Similarity 77.8%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231 GPLVCNGSL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Homo sapiens 'S-09-860-739-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GPLVCRGTL 9
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S-09-860-739-5
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Search completed: March 1, 2004, 18:08:52
Tob time : 24.1111 secs

8 GPLVCNGVL 16

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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| protein - protein search, using sw model

March 1, 2004, 17:21:01; Search time 10.2222 Seconds no m

(without alignments) 84.690 Million cell updates/sec

US-09-905-083-80 .tle: arfect score:

1 GPLVCRGTL 9 :donence: BLOSUM62 Gapop 10.0 , Gapext 0.5 coring table:

283366 segs, 96191526 residues

stal number of hits satisfying chosen parameters:

inimum DB seq length: 0

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* atabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	serine proteinase	semenogelase (EC 3	tissue kallikrein	probable aminoglyc	hypothetical prote	×	complement factor	semenogelase (EC 3	glandular kallikre	tissue kallikrein	Å	tissue kallikrein	ā	le B	kallikrei	(EC 3	9	$\ddot{a}$	kallikrein, glandu	chymotrypsin-like	'	tonin (EC 3.4.21	<pre>kalli</pre>	tissue kallikrein	neuropsin - mouse	tissue kallikrein	7S nerve growth fa	esne	tissue kallikrein
ID	A53968				G72548				I49	¥			B32340						S15685					A29746		KQMS1		•	A34079
Length DB	53	9	61	62		10	١n	_		10		ın	m	10	σ.	0	_	===	0	***	m	m.	m	<sub>መ</sub>	260 2	_	~	_	_
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Score	50	40			39	39	38	38	37	37	37	37	37	37	37	37	37	3.7	37	37	3.7	37	37	37	37	37	3.7	37	37
esult No.	-	a	m	4	S	9	7	σο	σ				13		15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

semenogelase (EC 3.4.21.77) precursor [validated] - human
NyAlternate names: gamma-seminoprotein; P-30 antigen; prostate-specific antigen; prostate.
C;Species: Homo saptens (man)
C;Date: 19-may-2000 #sequence revision 19-May-2000 #text change 08-Dec-2000
C;Accession: A32297; A32423; S03604; S05468; S05467; A32546; S02239; A26757; C31567; A31:
R;Riegman, P.H.J.; Vlietetra, R.J.; van der Korput, J.A.G.M.; Romijn, J.C.; Trapman, J.
B;Ochem. Biophys. Res. Commun. 159, 95-102, 1989
A;Title: Characterization of the prostate-specific antigen gene: a novel human kallikren:
A;Accession: A32297; MUID:89165891; PMID:2466464
A;Accession: A32297; MUID:89165891; PMID:2466464
A;Accession: A2229
A;Restdues: 1-261 «RIE»
A;Cross-references: GB:M24543
R;Lundwall, A.
Biochhem Biophys: Res. Commun. 161, 1151-1159, 1989
A;Title: Characterization of the gene for prostate-specific antigen, a human glandular k, A;Reference number: A32423; MUID:89302090; PMID:2472789

tissue kallikrein	gamma-renin (EC 5.	tissue kallikrein	tissue kallikrein	tissue kallikrein	granzyme 3 (EC 3.4	riboflavin biosynt	kallikrein - mouse	elastase (EC 3.4.2	tissue kallikrein	duodenase - bovine	trypsin (EC 3.4.21	trypsin (EC 3.4.21	_	snake venom factor
801971	AZBUBZ	A29745	845303	S15686	565663	T12994	152972	S44462	KQMSM	869370	TRDFS	TRPGTR	531778	A32121
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261	707	261	261	263	264	599	99	73	149	226	229	231	231	236
74.0	7 7	74.0	74.0	74.0	74.0	74.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0	72.0
37 74.0														

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R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T. J. Biol. Chem. 269, 19420-19426, 1994
J. Biol. Chem. 269, 19420-19426, 1994
J. Fitle: Clohing, expression, and characterization of stratum corneum chymotryptic enzym. A;Reference number: A53968; MUID:94308225; PMID:8034709
A;Accession: A53968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                           serine proteinase SCCE precursor - human
N'Alternate names: stratum corneum chymotryptic enzyme
C'Species: Homo sapiens (man)
C'Date: 07-Jul.1995 #sequence_revision 07-Jul-1995 #text_change 22-Jun-1999
C'Accession: AS3968
                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mENA
A;Reddues: 1-253 <HAN>
A;Coss-references: GB:L33404; NID:g521214; PIDN:AAC37551.1; PID:g532504
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Match 100.0%; Score 50; DB 2; Length 253; Local Similarity 100.0%; Pred. No. 0.085; loss 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Cross-references: GDB:377730
Map position: 7435-7435
C.Superfamily: trypsin, trypsin homology
F:30-245/Domain: trypsin homology TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 GPLVCRGTL 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: PRSS6; SCCE
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Matches
RESULT 1
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NiAlternate names: glandular kallikrein
C;Species: Homo sapiens (man)
C;Accession: A22586
R;Schedlich, L.J.; Bennetts, B.H.; Morris, B.J.
DNA 6, 429-437, 1987
A;Title: Primary structure of a human glandular kallikrein gene.
A;Reference number: A29586; MUID:88054467; PMID:2824146
A;Reference number: A29586; MUID:8805467; PMID:2824146
A;Reference number: A29586; MUID:8805467; PMID:2824146
A;Residues: 1-261 <<Schape A380586; A38058640; PIDN:AAA74454.1; PID:g386842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Molecule type: protein
A, Residues: 25-30, XX, 32-49 < CHR>
A, Residues: 25-30, XX, 32-49 < CHR>
C, Comment: This enzyme preferentially cleaves after tyrosine residues.
C, Comment: This enzyme preferentially cleaves after tyrosine residues.
C, Genetics:
A, Gene: GDB:APS; PSA
A, Cross-references: GDB:119695; OMIM:176820
A, Map position: 19913.3-19913.3
A. Introns: 16/1; 69/2; 165/1; 210/3
C, Superfamily: trypsin, trypsin, homology
C, Keywords: glycoprotein; hydrolase; predicted <SIG>F;11-17/Domain: signal sequence #status predicted <SIG>F;11-17/Domain: signal sequence #status predicted <SIG>F;18-24/Domain: sropeptide #status specificed <SIG>F;25-261/Product: semenogelase #status experimental <MAT>F;25-253/Domain: trypsin homology <TRY>F;65,120,213/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue kallikrein (EC 3.4.21.35) hGK-1 precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 77.8
Matches 7; Conservative
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Accession: A32423
Status preliminary
Molecule type: DNA
Residues: 1-261 <LUN>
Cross-references: GBNM27274; NID:g190552; PIDN:AAA60192.1; PID:g190553
Cross-references: GBNM27274; NID:g190552; PIDN:AAA60192.1; PID:g190553
D1gby, M.; Zhang, X.Y.; Richards, R.I.
Title: Acids Res. 17, 2137, 1989
Title: Human prostate specific antigen (PSA) gene: structure and linkage to the kallik
Accession: S03604
NUID:89183632; PMID:2467258
Accession: S03604
Reference in DNA
Residues: 1-261 cDIG>
Cross-references: EMBL:X13940
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A,Molecule type: mRNA

MyResidues: 5-164, CTPGPDGAAGSPDAWV <RI4>

A,Cross-references: GB:MZ1897; NID:9189529; PIDN:AAAS9997.1; PID:9189530

A,Note: the authors translated the codon GGC for residue 28 as Arg, TGG for residue 29 a

A,Schallar, J.; Akiyama, K.; Favida, R.; Hara, M.; Marti, T.; Rickli, E.E.

Bur, J. Biochem. 170, 111-120, 1987

A,Title: Isolation, characterization and amino-acid sequence of gamma-seminoprotein, a g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: mRNA

"Readues: 1-72,"T',74-85,"I',87-174,"P',176-183,"Q',185-259,"D',261 <HEN>
"Scalerences: GB:M2663

"Schulz, P.; Stucka, R.; Feldmann, H.; Combriato, G.; Klobeck, H.G.; Fittler, F.
uclaic Acids Res. 16, 6226, 1988

"Titler sequence of a cDNA clone encompassing the complete mature human prostate specifices enumber: S02239; MUID:88289366; PMID:2456523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Cross-references: EMBL:X14810;Henttu, P.; Vihko, P.; Volko, P.; Jenttu, P.; Vihko, P.; Commun. 160, 903-910, 1989;Jtle: Biophys. Res. Commun. 160, 903-910, 1989;Jtle: cDNA coding for the entire human prostate specific antigen shows high homologie;Reference number: A32546; MUID:89246551; PMID:2470373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.Cross-references: GB:M21895; NID:9189523; PIDN:AAA59995.1; PID:9189524
N/Note: the authors translated the codon GGC for residue 28 as Arg and TGG for residue
N/Accession: A31567
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1;Residues: 5-210, WVILITELIMPA',223,'PMVLHGSLV',233,'WRGGV' <RI3>
4;Cross-references: GB:M21896; NID:g189525; PIDN:AAA5996.1; PID:g189526
4;Note: the authors translated the codon GGC for residue 28 as Arg and TGG for residue
4;Accession: B31567
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Wolcaule type: MRNA
WARNA
WAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: DNA; Residues: 1-261 «KL1»; Richer, F. (2008-references: Embriato, G.; Schulz, P.; Arbusow, V.; Fittler, F. acleic Acids Res. 17, 3981, 1989; Titler Genomic sequence of human prostate specific antigen (PSA).; Reference number: S05467; MUID:89282407; PMID:2471958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;Molecule type: mRNA
.;Residues: 17-63, TT',65-135,'M',137-261 <SCH>
.;Crose-references: EMB:X07730
.;Lundwall, A.; Lilja, H.
EMB Lett. 214, 317-322, 1987
.;Title: Molecular clouing of human prostate specific antigen cDNA.
.;Reference number: A26757; MUID:87190978; PMID:2436946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klobeck, H.G.; Combriato, G.; Schulz, P.; Arbusow, V.; Fittler, inmitted to the EMBL Data Library, May 1989 Reference number: S05468
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Molecule type: DNA Residues: 1-29 <XL2>

Accession: A32546

Accession: S05468

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1; Molecule type: mRNA 1; Residues: 5-261 <RI2>

1, Accession: C31567

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Lissue kallikrein (EC 3.4.21.35) precursor - rat
NyAlternate names: glandular kallikrein; kininogenin; true tissue kallikrein
NyAlternate names: glandular kallikrein; kininogenin; true tissue kallikrein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Apr-1983 #sequence revision 05-Apr-1983 #text change 16-Jun-2000
C;Accession: A00944; A41429; A25137; UX0073; A23863; A33359
R;Swift, G.H.; Dagorn, J.C.; Ashley, P.L.; Cummings, S.W.; MacDonald, R.J.
Proc. Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982
A;Title: Rat pancreatic kallikrein mRNA: nucleocide sequence and amino acid sequence of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: mRNA
;Residues: 115-265 <GER>-
;Inoue, H.; Fukui, K.; Miyake, Y.
Elochem. 105, 834-840, 1989
;Title: Identification and structure of the rat true tissue kallikrein gene expressed in
;Reference number: JX0073; MUID:89327211; PMID:2753879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-265 <SWI>
A; Experimental source: pancreatic
A; Experimental source: pancreatic
A; Experimental source: pancreatic
A; Kato, H.; Nakanishi, E.; Enjyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biochem. 102, 1389-1404, 1987
A; Title: Characterization of serine proteinases isolated from rat submaxillary gland: wit A; Reference number: A41429; MUID: 88198057; PMID: 3482210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AjStatus: preliminary
AjMolecule type: protein
AjResidues: 29-53, 74, 55-87 «KAT»
RjGerald, W.L.; Chao, J.; Chao, L.
Bjöchim. Bicophya. Acta 866, 11-44, 1986
AjTitle: Immunological identification of rat tissue kallikrein cDNA and characterization
AjReference number: A25137; MUID:86131678; PMID:3004582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ashley, P.L.; MacDonald, R.J.
iochemistry 24, 4512-4520, 1985
.Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of
?Reference number: A22863; MUID:86051477; PMID:2998455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA

A; Residues: 1-265 < ASH:

A; Cross-references: GBH:

A; Cross-references: GBH:

A; Experimental source: submaxillary gland

A; Experimental source: submaxillary gland

A; Experimental source: submaxillary gland

A; Mines, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; MacDonald, R.J.

G. Biol. Chem. 264, 7653-7662, 1989

A; Title: Organization and expression of the rat kallikrein gene family.

A; Reference number: A33359; MUID: 89214217; PMID: 2708383
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C;Genetics:
A;Introns: 20/1; 73/2; 16/1; 214/3
C;Genetics: 20/1; 73/2; 16/1; 214/3
C;Superfamily: trypsin homology
A;Introns: 20/1; 73/2; 16/1; 214/3
C;Superfamily: trypsin; trypsin homology
F;10-28/Domain: signal sequence #status predicted <AP7-F;10-28/Domain: activation peptide #status predicted <AP7-F;29-26/Product: tissue kallikrein, pancreatic #status predicted <MP7-F;29-26/Product: tissue kallikrein, pancreatic #status predicted <MP7-F;29-26/Product: tissue kallikrein, pancreatic #status predicted F;35-177,54-70,156-223,188-202,213-238/Disulfide bonds: #status predicted F;69,124,217/Active site: His, Asp, Ser #status predicted
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;Cross-references: GB:D00448; NID:g220792; PIDN:BAA00346.1; PID:g220794
;Experimental source: kidney
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;Species: Aeropyrum pernix
;Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
;Accession: G72548
yka warabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah wa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Janazaki, J.; NA Res. 6, 83-101, 1999
*Yifile: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyi A; Accession: G72548
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A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1675
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Note: the authors translated the codon TAC for residue 43 as Trp Genetics:
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Best Local Similarity 77.8%; Pred. No. 5.8;
Matches 7; Conservative 1; Mismatches 1; Indels
                                                                             Introdes: 16/1; 69/2; 165/1; 210/3
Superfamily: trypsin; trypsin homology
Keywords: hydrolase; serine proteinase
25-253/Domaln: trypsin homology <TRY>
65,120,213/Active site: His, Asp, Ser #status predicted
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Best Local Similarity 88.9<sup>5</sup>
Matches 8; Conservative
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ACESON FINITION (EC 3.4.21.35), submandibular mGK-2 - mouse (fragment)
NyAlternate names: glandular kallikrein
Cispecies: Mus musculus (house mouse)
Cispecies: Musculus (sequence_revision 05-Jun-1987 #text_change 22-Jun-1999
Ciscession: AG5308
R;Mason, A.J.; Evans, B.A.; Cox, D.R.; Shine, J.; Richards, R.I.
Axitile: Structure of mouse kallikrein gene family suggests a role in specific processing
A;Reference number: A00941; MUID:83219214; PMID:6602295
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A;Residues: 1-96 <MAS>
A;Cross-references: GB:V00829; NID:g52775; PIDN:CAA24212.1; PID:g388523
A;Experimental source: Quakembush inbred strain
A;Note: this sequence has been translated from two exons (11-147 and 522-674) located ups
C;Comment: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release
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Jacobider Rallikrein - western wild mouse (fragment)
C;Bacies: Mus spretus (western wild mouse)
C;Bacies: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
C;Accession: 144416
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Reference number: 148934; MUID:94319082; PMID:8043949
A;Recession: I49416
A;Accession: J49416
A;Accession: J4941
                                        C.) Accession: S35711, S34239

R. Gauthher, E.N.; Chapdelaine, P.; Tremblay, R.R.; Dube, J.Y.

Biochim. Biophys. Acta 1174, 207-210, 1993

A. Title: Characterization of rhesus monkey prostate specific antigen cDNA.

A.) Reference number: S35711, MUID: 93363642; PMID: 7689340

A.) Recession: S35711

A.) Molecule type: mRNA

A.) Residues: L-561 - CADA.

A.) Residues: L-561 - CADA.

C.) Comment: This enzyme preferentially cleaves after tyrosine residues.

C.) Comment: This enzyme preferentially cleaves after tyrosine residues.

C.) Comment: This enzyme preferentially cleaves after tyrosine residues.

C.) Superfamily: trypsin homology creates; serine proteinase

F; 1-17/Domain: signal sequence #status predicted <SIG>
F; 18-24/Domain: propeptide #status predicted <RRO>
F; 25-253/Domain: trypsin homology <RRX>
F; 55-253/Domain: trypsin homology <RRX>
F; 65, 120, 213/Active site: His, Asp, Ser #status predicted
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Pred. No. 14;
0; Mismatches 2; Indels
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                 Species: Macaca mulatta (rhesus macaque)
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Best Local Similarity 77.8%;
Matches 7; Conservative
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es 6; Conserv
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Alternate names: adipsin; C3 convertase activator
Species: Homo sapiens (man)
Species: Homo sapiens (man)
Accession: A40197, A00936; A60571; S66645
White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S.;
Biol. Chem. 267, 9210-9213, 1992
Title: Human adipsin is identical to complement factor D and is expressed at high leve
Reference number: A40197; MUID:92250520; PMID:1374388
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;Title: Inhibition of degranulation of human polymorphonuclear leukocytes by complement;Reference number: $66645; MUID:96013156; PMID:7556615
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,Status: preliminary
Molecule type: protein
,Residues: 19-44, CC, 46-48 «BAL»
;Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, activ
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) Superfamily: trypsin; trypsin homology
) Superfamily: trypsin; trypsin homology
); Superfamily: trypsin; trypsin homology
); Reywords: complement alternate pathway; hydrolase; plasma; serine proteinase
); 13-246/Domain: signal sequence #status predicted <SIG>
); 13-246/Product: complement factor D (fragment) #status experimental <NAT>
); 13-246/Product: complement factor D (fragment) #status predicted
); 14-60,141-207, 172-188, 197-222/Josulfide bonds: #status predicted
); 59,105,201/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: GB;M84526
:Nlemann, M.A.; Bhown, A.S.; Bennett, J.C.; Volanakis, J.E.
lochemistry 23, 2482-2486, 1984
:Title: Amino acid sequence of human D of the alternative complement pathway.
Reference number: A00936; MUID:85000441; PMID:6383466
                                                                                                                         0; Gaps
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     78.0%; Score 39; DB 1; Length 265; 66.7%; Pred. No. 9.4; ative 1; Mismatches 2; Indels
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76.0%; Score 38; DB 1; Length 246;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 2; Indels
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Query Match
Sest Local Similarity 66.74
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                  219 GPLICNGVL 227
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Gaps

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C, Superfamily: trypsin, trypsin homology C, Keywords: hydrolase; serine proteinase
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: protein
A,Residues: 1-23:24-51;52-104 <GUT>
A;Residues: 1-23:24-51;52-104 <GUT>
A;Residues: 1-23:24-51;52-104 <GUT>
C;Respectamental source: submaxillary gland
C;Superfamily: trypsin; trypsin; nomology
C;Reywords: hydrolase; serine proteinase
P;1-104/Domain: trypsin homology (fragments) <TRY>
P:1-104/Domain: trypsin homology (fragments) <TRY>
P:1-23/Product: tissue kallikrein-related protein kl0 heavy chain (fragment) #status exp
P;24-51/Product: tissue kallikrein-related protein kl0 heavy chain (fragment) #status exp
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NiAlternate names: glandular kallikrein; kininogenin

(), Alternate names: glandular kallikrein; kininogenin

(), Date: 22-Uul-1987 #sequence_revision 22-Jul-1987 #text_change 22-Jun-1999

(), Date: 22-Uul-1987 #sequence_revision 22-Jul-1987 #text_change 22-Jun-1999

R), Ashley, P.L.; MacDonald, R.J.

Biochemistry 24, 4512-4520, 1985

By, Ashley, P.L.; MacDonald, R.J.

AyAccession: B23863, MUID:86051477; PMID:2998455
                                                        Junicons: 45/3
Superfamily: trypsin; trypsin homology
;Keywords: glycoprotein; hydrolase; saliva; serine proteinase; submandibular gland
';1-88/Domain: trypsin homology (fragment) <TRX>
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A;Residues: 1-156 <A&H>
A;Cross-references: GB:Mil564; NID:g205031; PIDN:AAA41465.1; PID:g205032
C;Superfamily: trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-148/Domain: trypsin homology (fragment) <TRY>
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                                                                                                                                                                                                    74.0%; Score 37; DB 2; Length 96; ilarity 66.7%; Pred. No. 8.8; Conservative 1; Mismatches 2; Indels
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                               Map position: 7
Gene: mGK-2
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C;Accession: B32340
R;Shai, S.Y.; Woodley-Miller, C.; Chao, J.; Chao, L.
Biochemistry 28, 5334-5343, 1989
A;Title: Characterization of genes encoding rat tonin and a kallikrein-like serine prote
A;Reference number: A32340; WUID:89375248; PMID:2550051
                                                                                                                                                                                                                                                                                                 A Accession: B32340
A Status: preliminary
A)Molecule type: DNA
A)Molecule type: DNA
A)Residues: 1-188 <BHA>
A)Cross-references: GB:MA6534; NID:g206773; PIDN:AAA42080.1; PID:g206774; GB:J02860
C;Superfamily: trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-180/Domain: trypsin homology (fragment) <TRY>
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C:Daces 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 19-May-2000
C:Dacession: S45356
R:Dihanich, M.; Spiess, M.
Biochim. Bacohim. Acra 1218, 225-228, 1994
A:Title: A novel serine proteinase-11ke sequence from human brain.
A:Reference number: S45356; MUID:94289486; PMID:8018728
tissue kallikrein (EC 3.4.21.35) 3 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1989 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue kallikrein (EC 3.4.21.35), prostatic - guinea pig
Altlernades names: glandular kallikrein
Cispecies: Cavia porcellus (guinea pig)
Cibate: 08-Mar-1999 #sequence_revision 08-Mar-1989 #text_change 01-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1.-25 ADIH-
A;Cross-references: EMBL:X75363; NID:g407137; PIDN:CAA53145.1; PID:g940540
A;Experimental source: Alzheimer's disease patient brain cortex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable serine proteinase (EC 3.4.21.-) ACO - human (fragment)
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Biochemistry 26, 3471-3478, 1987
A;Title: Amino acid sequence of guinea pig prostate kallikrein.
A;Reference number: A27207; MUID:88000549; PMID:3307909
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Residues: 1-239 <DUN>
Note: 50-Trp was also found
Superfamily: trypsin, trypsin homology
Keywords: hydrolase; serine proteinase
1-231/Domain: trypsin homology <TRX>
41,96,191/Active site: His, Asp, Ser #status predicted
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0; Gaps Query Match 74.0%; Score 37; DB 2; Length 239; Best Local Similarity 66.7%; Pred. No. 20; Matches 6; Conservative 1; Mismatches 2; Indels

1 GPLVCRGTL 9

Parch completed: March 1, 2004, 17:36:31 b time : 11.3333 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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| protein - protein search, using sw model

March 1, 2004, 17:17:25; Search time 6 Seconds (without alignments) 78.105 Million cell updates/sec no u

US-09-905-083-80 50 1 GPLVCRGTL 9 tle: trfect score: squence:

oring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

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141681 stal number of hits satisfying chosen parameters:

inimum DB seg length: 0 aximum DB seg length: 2000000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase ;

SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	рошо	homo	Q9p0g3 homo sapien	both	ratti	homo	з пото	rattı	пошо	пошо	mus n	trime	homo	macac	рошо	рошоц	homo	พนธ ท			cavia	gadus	_		halic	homo sa	9h2r5 homo	54 rattus	P00759 rattus norv	17 ratt	948 mus	55 mus	75
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P109756 mus musculu P15945 mus musculu P15947 mus musculu P36374 rattus norv P15949 mus musculu P15946 mus musculu P04071 mus musculu P34284 pracomys nat P49863 homo sapien P37358 equus cabal
KLK3 MOUSE KLK5 MOUSE KLK8 RAUSE KLK8 RAT KLK9 MOUSE KLK8 RAUSE KLKG WOUSE KLKG WOUSE GRAK MOUSE GRAK HUMAN KLKO HUMAN ELZD HUMAN
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261 261 261 261 261 274 274
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## ALIGNMENTS

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cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-|-Tyr-25, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines.

--- TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Very low levels are also seen in the brain and kidney.

---- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.

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16-007-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KLK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
WALKED (GLCNAC. . .) (POTENTIAL).
WALKED (GLCNAC. . .)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MIN, 004438; C. Serine-type peptidase activity, TAS. GO; GO:000824; P:serine-type peptidase activity, TAS. GO; GO:0008544; P:epidermal differentiation, TAS. INTERPROPOSE OF SERVICE TEXPORTS.

INTERPROPER OF SERVICES OF SER
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EMBL; AF166330; AAD49718.1; --
EMBL; AF32589; AAG9624.1; --
EMBL; A53968; A53968.
PIR; A53968; A53968.
MESSP; 900763; 1DPO.
MEROPS; S01.300; --
Genew; HGNC:6368; KLK7.
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KLK9 HUMAN
ID KLK9 HUMAN
AC QSUKQ9;
DT 16-OCT-2001
DT 28-FEB-2003
DE KAllikrein 9
DE LI3).
GN KLK9.
CS HOMO Sapiens
OC Bukaryota; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Brant. Jeasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
Danganan L., Stier A., Christensen M., Georgescu A., Avila J., Liu S.,
Andreise T., Trankheim M., Attix C., Amico-Keller G., Coeffield J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Carrano A.V.,
"Sequence analysis of chromosome 19q13.4.",
"Sequence analysis of thromosome 1
                                                                                                                                                                                                                                                                                                                   MEDLINE-20247258; PubMed=10783266;
Yousef G.M., Diamandis E.P.;
"The expanded human kallikrein gene family: locus characterization and molecular cloning of a new member, KLK-L3.";
Genomics 65:184-194(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINES-20118156, PubMed=10652563;
Yousef G.M., Luo L.-Y., Diamandis B.P.;
"Identification of novel human kallikrein-like genes on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PÖTENTIAL.
KALLIKREIN 9.
CHARGE RELAY SYSTEM (BY SIMILABITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paeper B., Wang K.;
"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";
Gene 257:119-130 (2000)
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R WRROPS, 2013.307, LDFU.

R Genew, HGNC: 6370, KLK9.

MIM, 605504, C:extracellular, NAS.

GO; GO:0005252; F:serine-type endopeptidase activity; NAS.

GO; GO:0005208, P:proteolysis and peptidolysis, NAS.

InterPro, PRR001254; Peptidase S1.

InterPro, IPR001254; Peptidase S1.

R PEANTS; PR00722; CHYWORTYPSIN.

R PRANT; SMO0722; CHYWORTYPSIN.

R PROSITE; PS50240; TRYPSIN LDM; I.

R PROSITE; PS50134; TRYPSIN LDM; I.

R PROSITE; PS00134; TRYPSIN LBF; I.

R PROSITE; PS00134; TRYPSIN LBF; I.

R Hydrolase; Serine protesse; Glycopetein; Signal.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                         19913.3-913.4.";
Anticancer Res. 19:2843-2852(1999).
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Burkhart-Schultz K., Gordon L., Dias J., Ranirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
Andreise T., Trankheim M., Attix C., Amico-Keller G., Coeffeld J.,
Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Sequence analysis of chromosome 19q13.4.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification and characterization of KLK14, a novel kallikrein serine protease gene located on human chromosome 19q13.4 and expressed in prostate and skeletal muscle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIATE=205447, PubMed=10969073;

MEDIATE=2054474, PubMed=10969073;

MEDIATE=2054474, PubMed=10969073;

Clements J.A.;

Clements J.A.;

"Tisque-specific expression patterns and fine mapping of the human fall-krain (KLK) locus on proximal 19413.4.";

J. Biol. Chem. 275:3737-37406(2000)

-: STBCELLIATAR LOCATION: Secreted (Probable)

-: STBCELLIATAR LOCATION: Secreted (Probable)

-: TISSUE SPECIFICITY: High expression in brain, bone marrow and fetal liver. Also expressed in liver, pancreas, fetal spleen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yousef G.M., Diamandis E.P., mapping, and tissue expression of KLKL6, mMolecular characterization, mapping, and tissue expression of KLKL6, a hormonally regulated Mallikrein-like gene."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                      Gaps
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLXLA OR KLXL6.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last amnotation update)
Kallikrein 14 precursor (EC 3.4.21.-) (Kallikrein-like protein 6)
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                                                                                                                                                                                                                 90.0%; Score 45; DB 1; Length 250;
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MEDILIPE-1250997; Pubmed=1135573;
HOOPER J.D., Bui L.T., Rae F.K., Harvey T.J., Myers S.A., Ashworth L.K., Clements J.A.)
                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                       27512 MW; F2785245B063E98B CRC64;
                                                                                                                                                                                                                                   Pred. No. 0.16;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 251 AA.
                                                                                                                                                                                                                                   88.98;
                                                                                                                                                                                                                                   Local Similarity 88.9
nes 8, Conservative
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                                                                                                                             131
166
211
250 AA;
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-i- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.

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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 41, Last annotation update)
Venom serine proteinase A precursor (BC 3.4.21,-).
Bothrops jararaca (Jararaca).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                   R HSDP FOOTS 1 1DPD.

R HSDP FOOTS 1 1DPD.

R HSDP FOOTS 1 1DPD.

R Genew, FONC 5362; KLK14.

MIN; 606135; ---

GO; GO:0004525; F:serine-type endopeptidase activity; NAS.

GO; GO:0004525; F:serine-type and peptidolysis; NAS.

GO; GO:0004508; P:protecolysis and peptidolysis; NAS.

R DITERPRO; IPRO1354; Peptidase_S1.

R InterPro; IPRO1354; Peptidase_S1.

R InterPro; IPRO1354; Peptidase_S1.

R PROSTITS; PRO0320; LYPSIN, 1.

R PROSTITS; PSO0320; TRYPSIN DCM; 1.

R PROSTITS; PSO0335; TRYPSIN DCM; 1.

R PROSTITE; PSO0135; TRYPSIN HIS; 1.

R PROSTITE; PSO0135; TRYPSIN HIS; 1.

R POTENTIAL.

T CHALIN 25 STINE POTENTIAL.

T CHALIN 25 STINE NASHINGER; NA CHANTAN ACTIVATION PEPTIDE (POTENTIAL).

T CHALIN 25 STINE FOUNDER; NA CHANTAN ACTIVATION PEPTIDE (POTENTIAL).

T CHALIN 25 STINE NASHINGER; NA CHANTAN ACTIVATION PEPTIDE (POTENTIAL).

T CHALIN 25 STINE NASHINGER; NA
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Thrombin-like snake venom serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9087953BAFA7ED25 CRC64;
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prostate and skeletal muscle
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TISSUE=Venom gland;
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SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110
260 AA;
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CHAIN
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DISULFID
CARBOHYD
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                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: Belongs to peptidase family S1. Snake venom subfamily.
                                                                                                                                                                                                                                                                                                                rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine procease 1).
KLK8 OR PRSS19 OR NRPN OR BSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%; Score 40; DB 1; Length 258; 75.0%; Pred. No. 1.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                              EMBL; AB031394; BAA89310.1; -.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Fischer, TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 75.0 les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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206 GPLICNGT 213
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                                                                                                                                                                                                                                                                                                            MEROPS; S01.181;
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TRENT RAT
TO ON8 780;
TO 15-UT-199
TO 28-F2B-200
TO 15-UTL-199
TO 28-F2B-200
TO Neuropsin
TO Neurops
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NEDLINE=98389725; PubMed=9722524;
Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;
Serine proteages in rodent hippocampus.";
J. Biol. Chem. 273:23004-23011(1998).
-! FUNCTION: Suggested to be involved in kindling epileptogenesis and hippocampal plasticity. Has a strong proteolytic activity against fibronectin (By similarity).
-! CATALITIC ACTIVITY: Preferential cleavage: Arg., Lys...
-! SUBLEBLULAR LOCATION: Secreted (By similarity).
-! SINCELLULAR LOCATION: Secreted (Lysimilarity).
-! SINCELLULAR LOCATION: Secreted (Lysimilarity).
-! SINIARTY: Belongs to peptidase family SI. Kallikrein subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 N-LINKED (GLCNAC. . .) (POTENTIAL).
28510 MW; 58DF4F0602A0B7F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R MELPA MODOS 41, CAA06643.1; -...
R HSSP; Q6195; INPM.
R MEROPS; S01.244; -...
R InterPro; IPR001254; Peptidase_S1.
R InterPro; IPR001254; Peptidase_S1.
R InterPro; IPR001254; Peptidase_S1A.
R PEAM, PR00039; Trypsin, Peptidase_S1A.
R RRINTS; PR00020; Trypsin, Dow; R PROSITE; PS00134; TRYPSIN Dow; PROSITE; PS00134; TRYPSIN Dow; R PROSITE; PS00134; TRYPSIN Dow; R PROSITE; PS00135; TRYPSIN SIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.0%; Score 40; DB 1; Length 260;
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NEUROPSIN.
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of human genes.";
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      THE HELLE LELECT OCCUPANTA TO THE PROPERTY OF 
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MEDLINE=228825; Pubmed=12477932;

REDLINE=228825; Pubmed=12477932;

RIABSERS R. Collins F.S., Hagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,

Antschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Bhat N.K.,

Antschul S.F., Zeeberg B., Buetow K.H., Schefer C.F., Haieh F.,

Antschul S.F., Zeeberg B., Buetow K.H., Schefer T.F.,

Antschul S.F., Zeeberg B., Buetow K.H., Rang J., Hsieh F.,

Antschul S.F., Jordan H., Morer T. Mang J., Hsieh F.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Frange C.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Basak S.A., McEwan P.J., McKernan K.J., Andlek J.A., Gubbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Anthing M., Madan A., Sodergren E.J., Lu X., Gibbs R.A.,

Faley J., Helton E., Ketteman M., Sodergren S.J., Lu X., Gibbs R.A.,

Rakelley R.W., Touchman J.W., Ghan A., Rodrigues S., Sanchez A.,

Balkeeley R.W., Touchman J.W., Gchmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Anthing M., Madan A., Schmutz J., Myerz R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Anthing M., Madan A., Schmutz J., Myerz R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Anthing M., Madan A., Schmutz J., Myerz R.M.,

Butterfield W.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Center C.M., Madan S., Wong G., Schmutz J., More than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=20012757; PubMed=10544017;
Liu X.F., Essand M., Vasmatzis G., Lee B., Pastan I.;
"Identification of three new alternate human kallikrein 2 transcripts:
evidence of long transcript and alternative splicing.";
Biochem. Biophys. Res. Commun. 264:833-839(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Characterization of single-nucleotide polymorphisms in coding regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K.J., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Attix C., Andreise T., Trankheim M., Georgescu A., Avila J., Liu S.,
Buarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
Arellano A., Brower A., Sanders C., Ow D., Nolan M., Trong S.,
"Sequence analysis of a 4.8 Mb region of 19q13.4 between KLKI and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99318093, PubMed=10391209,
Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lahe C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
Lander E.S.;
                                                                                                                                                                                                                                                                                 "Identification and androgen-regulated expression of two major human glandular kallikrein-1 (hGK-1) mRNA species."; Mol. Cell. Endocrinol. 76:181-190(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=20510030; PubMed=11054574; MEDLINE=20510030); PubMed=11054574; Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J. Moss P., Paeper B., Wang K.; "Sequencing and expression analysis of the serine protease gene cluster located in Chromosome 19q13 region."; Gene 257:119-130(2000).
                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUB=Prostate;
TISSUB=1726490;
Riegman P.H., Vlietstra R.J., der Korput H.A., Romijn J.C.,
Trapman J.;
                               Schedlich L.J., Bennetts B.H., Morris B.J.; "Primary structure of a human glandular kallikrein gene."; DNA 6:429-437(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
MEDLINE=88054467; PubMed=2824146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).
GDSGGPLVCNGVLQGITSWGPEPCALPEKPAVYTKVVHYRK
                                                                                                                                                                                                               in Kininogen to release Lys-bradykinin.
-!- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in small molecule substrates. Highly selective action to release kalidin (lysyl-bradykinin) from kininogen involves hydrolysis of Met-|-Xaa or Leu-|-Xaa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P20151-3; Sequence=VSP_005400;
SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interero; irruoil24; Peptidase_S1.
Interero; Irruoil24; Peptidase_S1A.
Pram; Protoid9; trypsin; Irruoil24; Peptidase_S1A.
Pram; Protoid9; trypsin; Irruoil25; CHYMOTRYPSIN.
SWART; SMG0020; Tryp_SPC; 1.
PROSITE; PSG0134; TRYPSIN_DOM; I.
PROSITE; PSG0135; TRYPSIN_BSR; 1.
Hydrolase; Serine protease; Glycoprotein; Multigene family; Zymogen; Signal; Alternative splicing; Polymorphism.
Incomp.
                                                                  Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim B.P., Kalyanaraman N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
                                                                                                                                                                      Nat. Genet. 23:373-373(1999).
-!- FUNCTION: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVATION PEPTIDE (PROBABLE).
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
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GO, GO:0004293; FitisBue kallikrein activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                             Event = Alternative splicing; Named isoforms = 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P20151-1; Sequence=Displayed;
Name=2; Synonyms=PGK-10A;
IsoId=P20151-2; Sequence=VSP_005399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC037199; -; NOT ANNOTATED_CDS. BC005196; AAH05196.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M18156; -; NOT_ANNOTATED_CDS.
EMBL; M18157; AAA7454.1; -.
EMBL; S39329; AAD13816.1; -.
EMBL; S39329; AAD13817.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF188745; AAF08275.1; -. AF188746; AAF08276.1; -. AF188747; AAF08277.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF243527; AAG33356.1; -
Nat. Genet. 22:231-238(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR, A29586; A29586.
HSSP; P07288; IPFA.
MEROPS; S01.161; ..
Genew; HGNC:6363; KLKZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lander E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                              Name=1;
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ACT_SITE
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DISULFID
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EMBL;
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EMBL;
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P07288; QL6272;
01-AZR-1988 (Rel. 07, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Prostate specific antigen precursor (RC 3.4.21.77) (PSA) (Gammaseminoprotein) (Kallikrein 3) (Semenogelase) (Seminin) (P-30 antigen).
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89183612; PubMed=2467258; Digby M.R., Zhang X.Y., Richard R.I.; Midman prostate specific antigen (PSA) gene: structure and linkage to the kallikrain-like gene, hGK-1."; Nucleic Acids Res. 17:2137-2137(1989).
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Characterization of the gene for prostate-specific antigen, a human
WIKDTIAANP -> VSHPYSQHLEGK (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=89246551; PubMed=2470373; Henttu P., Vihko P.; For the entire human prostate specific antigen shows icDNA coding for the entire human prostate specific antigen shows high homologies to the human tissue Kallikrein genes."; Biochem. Biophys. Res. Commun. 160:903-910(1989).
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klobeck H.-G., Combriato G., Schulz P., Arbusow V., Fittler F.; "Genomic sequence of human prostate specific antigen (PSA)."; Nucleic Acids Res. 17:3981-3981(1989).
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"Molecular cloning of human prostate specific antigen cDNA.";
FEBS Lett. 214:317-322(1987).
                                                                                             Score 40; DB 1; Length 261;
                                                                                                                  2; Indels
                  /FTIG=VSP 005399.
Nisaing (in isoform 3).
/FTIG=VSP 005400.
V -> L (in dbSNP:6072).
/FTIG=VAR 014164.
W, 9CF7P4Alle2EP42D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glandular kallikrein.";
Biochem. Biophys. Res. Commun. 161:1151-1159(1989).
                                                                                                       Pred. No. 1.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Leukocyte;
MEDLINE-89302090; PubMed=2472789;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=89282407; Pubmed=2471958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87190978; PubMed=2436946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Prostate;
MEDLINE=89165891; PubMed=2466464;
                                                                        28671 MW;
                                                                                        Query Match
Best Local Similarity 77.8%;
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                                                                                                                                                           215 ĠPĹVĊNĠVĹ 223
                                                                                                                                       1 GPLVCRGTL 9
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                                                                         261 AA;
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                               VARSPLIC
                                                                        SEQUENCE
                                                   VARIANT
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RESTREPROBLEMS, and Prostate;

MEDLINE=228.8257; PubMed=12477932;

Straubberg N.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riamberg R.L., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

A blatchenon M.J. Gadra M.F., Canadow M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J. Uedin T.B., Toshiyuki S., Carninci P., Prange C.,

A Rafa S.S., Loquillano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., McEwran K.J., Malek J.A., Gunaratne P.H.,

Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Morley K.C., Raderson E.J., Nordigues S., Sanchez A.,

A Richards M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W. Touchman J.W., Green E.D., Dickeon M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.;

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Reconstrain and intrial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-55079406; PubMed-757295; Monne M., Croce C.M., Yu H., Diamandis E.P.; Monne M., Croce C.M., Yu H., Diamandis E.P.; Molecular characterization of prostate-specific antigen messenger RNA
Riegman P.H.J., Vlietstra R.J., van der Korput J.A.G.M., Romijn J.C., "Characterization of the prostate-specific antigen gene: a novel human kallikrein-like gene."; Biochem. Biophys. Res. Commun. 159:95-102(1989).
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                                                                                                                                                                                                                                                                                                                                                                                 Monne M.M., Moreno J.M., Mele C.M., Mulholland G.M., Gomella L.G., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 25-261.
MEDLINE=8808286; PubMed=3691515;
MEDLINE=8808286; PubMed=3691515;
Schaller U., Akiyama K., Tsuda R., Hara M., Marti T., Rickli E.E.;
"Isolation, characterization and amino-acid sequence of gamma-seminoprotein, a glycoprotein from human seminal plasma.";
Eur. J. Biochem. 170:111-120(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE-20510330; PubMed=11054574; Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paeper B., Wang K.; Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19913 region."; Gene 257:119-130(2000).
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Schulz P., Stucka R., Feldmann H., Combriato G., Klobeck H.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 25-261.
MBDLINE=8620587; PubMed=2422647;
WALL K.W. K., Lee P.U., M'Timkulu T., Chan W.P., Loor R.;
"Human prostate-specific antigen: structural and functional and milarity with serine proceases.";
Proc. Natl. Acad. Sci. U.S.A. 83:3166-3170(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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us-09-905-083-80.rsp

A -> T (IN REF. 11).

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Conservative
                                                                                                                                              STANDARD;
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64
                                                                                       215 GPLVCNGVL 223
                                                                 1 GPLVCRGTL 9
                               Best Local Similarity
Matches 7; Conserv
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64
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                                                                                                                                 KLK1 RAT
ID KLK1 RAT
AC P00758;
CONFLICT
                       Query Match
                                           Matches
                                                                                                                       RESULT 8
                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its wase by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@lsb-sib.ch).
                                                                                                                                                       coagulum.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-| Xaa.
-!- SIMILARITY: Belongs to peptidase family $1. Kallikrein subfamily.
MEDLINE=95218633; PubMed=7535613;
Villoutreix B.O., Getzoff E.D., Griffin J.H.;
"A structural model for the prostate disease marker, human prostate-
                                                                          MEDLINE 98427950; PubMed=9751643;
Combs GS., Rergestrom R.C., Pellequer J.L., Baker S.I., Navre M., Smith M.M., Tainer J.A., Madison E.L., Corey D.R.;
"Substrate specificity of prostate-specific antigen (PSA).";
Chem. Biol. 5:475-488(1989)
-!- FUNCTION: Presumably hydrolyze the high molecular mass seminal vesicle protein thus leading to the liquefaction of the seminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolame, Serine proteame, Glycoprotein, Antigen, Zymogen, Signal,
3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTIVATION PEPTIDE.
PROSTATE SPECIFIC ANTIGEN.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO, GO:0008236; F:serine-type peptidase activity; TAS.
Interpro; IPR009003; Cys. Ser. trypsin.
Interpro; IPR001254; Peptidase Si.
Interpro; IPR001314; Peptidase_SiA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC. . .).
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                                                                                                                                                                                                                                                                                                                                                                        X07730; -; NOT ANNOTATED CDS.
M27274; AAA60192.1; -.
                                                                                                                                                                                                                                                                                                                  CAA32124.1; ALT SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN DOW; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
                                             Protein Sci. 3:2033-2044(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                      AAG33355.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                 BC005307; AAH05307.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          BC050595; AAH50595.2; -
                                                                                                                                                                                                                                                                                            EMBL; X14810; CAA32915.1; -. EMBL; X13940; CAA32123.1; -.
                                                                                                                                                                                                                                                                                                                                     X13943; CAA32126.1; -.
X13944; CAA32127.1; -.
X05332; CAA28947.1; -.
                                                                                                                                                                                                                                                                                                                             CAB46487.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , S01.162; -
HGNC:6364; KLK3.
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65
120
213
69
173
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                                                                   3D-STRUCTURE MODELING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1PFA; 26-JAN-95.
2PSA; 16-MAR-99.
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                                   specific antigen.";
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213
213
31
31
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1152
209
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                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
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Wines D.R., Brady J.M., Pritochett D.B., Roberts J.L., Macdonald R.J.;
"Organization and expression of the rat kallikrein gene family.";
J. Biol. Chem. 264:7653-7662(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Kidney;
MEDLINE-8932211; PubMed=2753879;
Inoue H., Fukui K., Miyake Y.;
"Identification and structure of the rat true tissue kallikrein gene expressed in the kidney.",
"Jacohem. 105:884-840(1899).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 48-261 FROM N.A.
MEDIATRE=86131678; PubMed=3004582;
GERAIG W.L., Chao L.,
"Immunological identification of rat tissue kallikrein cDNA and
characterization of the kallikrein gene family.";
Blochim. Blochim. Blochys. Acta 866:1-14 (1986).
i- FUNCTION: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=83117659; PubMed=6961406;
Swift G.H., Dagorn J.-C., Ashley P.L., Cummings S.W., McDonald R.J.;
"Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid
sequence of the encoded preproenzyme.";
Proc. Natl. Acad. Sci. U.S.A. 79:7263-7267(1992).
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Submaxillary gland;
MEDLINE=86051477; PubMed=2998455;
Ashley P.L., Macdonald R.J.;
AKAllkrein-related mRNAs of the rat submaxillary gland: nucleotide sequences of four distinct types including tonin.";
Biochemistry 24:4512-4520(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Glandular kallikrein, pancreatic 1 precursor (EC 3.4.21.35) (Tissue kallikrein) (PS kallikrein) (RGK-1)
                                                                      .
                                                              2; Indels
80.0%; Score 40; DB 1; Length 261; 77.8%; Pred. No. 1.6; 2; Indels.ive 0; Mismatches 2; Indels.
                                                                                                                                                                                                                                                                                                                                                                                  261 AA.
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                Primi, PRO089; LTypsin, Figurese_Sin.
Primis; PRO089; LTypsin, Interpresen.
PRIMIS; PRO0122; Trypsin, Interpresen.
PROSITE; PS00134; TRYPSIN, DOM; 1.
PROSITE; PS00134; TRYPSIN, BS; 1.
PROSITE; PS00134; TRYPSIN, BS; 1.
Hydrolase; Serine protease; Glycoprotein; Multigene family; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20118156; PubMed-10652563;
Yousef G.M., Luo L.-Y., Diamandis E.P.;
"Identification of novel human kallikrein-like genes on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UKRO; Q9UKRI;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein
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                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (PROBABLE)
F2F99C0227A7882B CRC64;
                                                                                                                                                                                                                                                                                           ACTIVATION PEPTIDE (PROBABLE).
GLANDULAR KALLIKREIN 1.
CHAIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 78.0%; Score 39; DB 1; Length 261; Best Local Similarity 66.7%; Pred. No. 2.5; Matches 6; Conservative 1; Mismatches 2; Indels
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BY SIMILARITY.
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                                      EMBL; J00758; -; NOT ANNOTATED CDS.
EMBL; M11563; AAA41464.1; ALT_INIT.
EMBL; M23874; AAA41462.1; JOINED.
EMBL; M23875; AAA41462.1; JOINED.
EMBL; M23875; AAA41462.1; JOINED.
EMBL; D00444; BAA03346.1; JOINED.
EMBL; D00444; BAA00346.1; JOINED.
EMBL; X03560; CAAZ7247.1; -.
HSRP, A00944; KQRTP.
HSRP, P00757; 1SGF.
                                                                                                                                                                    InterPro, IPR009003; Cys Ser trypsin.
InterPro, IPR001254; Peptidase_S1.
InterPro, IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                        PROBABLE
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Anticancer Res. 19:2843-2852(1999).
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28852 MW;
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152 2
184 1
209 2
108 1
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RESIDENCE FROM N.A. (ISOCORNS 1 AND 2). Diamendis E.P.,

YOURSE G.M., Madylarar A., Corolles A. Diamendis E.P.,

YOURSE G.M., Madylarar A., Corolles A. Diamendis E.P.,

RESIDENCE FROM N.A. (ISOCORNE 1).

RESIDENCE FROM N.A. (ISOCORNE 1).

MEDILAR-SOURCE FROM N.A. (ISOCORNE 1).

RESIDENCE FROM N.A. (ISOCORNE 2).

RESIDENCE FROM N.
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SIGNAL
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15-DEC-1998 (Rel. 37, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Complement factor D precursor (EC 3.4.21.46) (C3 convertase activator)
(Properdin factor D) (Adipsin).
BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

KYVDWIRMIMENN -> NSTLVGLGTSWNFNSCQPF (in
                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE OF 26-252.
MEDLINE-84109950; PubMed-6363133;
Obbison D.M.A., Gagnon J., Reid K.B.M.;
"Amino acid sequence of human factor D of the complement system.
Similarity in sequence between factor D and proteases of non-plasma
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 8-253 FROM N.A. MEDIATE-2920520; bubMed=1374388; MEDIATE-29250520; bubMed=1374388; White R.T., Dawm D., Hancock N., Rosen B.S., Lowell B.B., Usher P., Flier J.S., Spiegelman B.M.; "Human adippis is identical to complement factor D and is expressed at high levels in adippes tissue."; J. Biol. Chem. 267:9210-9213(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL SEQUENCE OF 26-61 AND 194-220.
MEDLINE=64256515; PubMed=6821372;
MEDLINE=64256515; PubMed=6821372;
MEDLINE=64256515; PubMed=6821372;

"Pactor D of the alternative pathway of human complement.

Purification, alignment and N-terminal amino acid sequences of the major cyanogen bromide fragments, and localization of the serine residue at the active site.;

Biochem. J. 187:863-874(1980).
                                                                                                                                                                                                                                                                                                                                nomo appress. Actacami, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                        Match 16.0%; Score 38; DB 1; Length 248; Local Similarity 77.8%; Pred. No. 3.7; Onservative 0; Mismatches 2; Indels
                                                                isoform 2).
/FTId=VSP 005403.
BB473E98F8BAF703 CRC64;
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MEDLINE-80145719; PubMed=6987665;
Volanakis J.E., Bhown A.S., Bennett J.C., Mole J.E.;
                                                                                                                                                                                                                                 253 AA
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                                                                                                                                                                                                                                 PRT;
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                                                                                        MW;
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FEBS Lett. 166:347-351(1984).
                                                                                         26733
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Matches
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The Secretal amino acid sequence of human factor Dihomology with serine processes. The Secretal amino acid sequence of human factor Dihomology with serine processes. The Secretary Secret

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STRAIN=BALB/C;

XX MEDLINE=97362044; PubMed=9211743;

A Aveskogh M., intralschwab C., Huang M.R., Hellman L.;

A Toweskogh M., intralschwab C., Huang M.R., Hellman L.;

AT "Characterization of coDNA clones encoding mouse proteinase 3

RI "Immunogenetics 46:181-1917(1997).

C. '- FUNCTION: Polymorphonuclear leukocyte serine protease that

CC degrades elastin, fibronectin, laminin, vitronectin, and collagen

CC ypes I, III, and IV (in vitro) and causes emphysema when

administered by tracheal insufflation to hameters (By similarity).

CC -- CATALYTIC ACTIVITY: Hydrolysis of proteins, including elastin, by

CC -- CATALYTIC Activity: Belongs to peptidase family SI. Blastase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99126347; PubMed=9925946; Sturrock A., Franklin K.F., Wu S.-Q., Hoidal J.R.; Carrock A., Franklin K.F., Wu S.-Q., Hoidal J.R.; Mouse proteinase-3 "Characterization and localization of the genes for mouse proteinase-3 (Prtn3) and neutrophil elastase (Ela2)."; Cytogenet. Cell Genet. 83:104-108(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=129/Sv;
MEDLINE=973029; PubMed=9187364;
Jenne D.E., Froehlich L., Hummel A.M., Specks U.;
"Cloning and functional expression of the murine homologue of proteinase 3: implications for the design of murine models of
                                                                                                                                                                                                                PRN3 MOUSE STANDARD; PRT; 234 AA.
28-1056; 008809;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Myeloblastin precursor (EC 3.4.21.76) (Proteinase 3) (PR-3).
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                                                                                      210 ĠPĽVĆGĠVĽ 218
                                  1 GPLVCRGTL 9
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STRAIN=129/SvJ;
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H -> F (IN REF. 6).
M -> V (IN REF. 6).
H -> E (IN REF. 4 AND 5).
G -> A (IN REF. 1 AND 2).
C -> R (IN REF. 1 AND 2).
S -> T (IN REF. 1 AND 2).
S -> T (IN REF. 4).
HSES. -> TILP (IN REF. 4).
HSSING (IN REF. 4).
TCNRRTHHOGALTE -> KCRLYDVL (IN REF. 4).
MISSING (IN REF. 3).
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     CHARGE RELAY SYSTEM.
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253 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MENOPS, SOL1134; -...
MED, MG1:89580; Prtn3.
MGD, MG1:89580; Prtn3.
InterPro; IPR001204; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
Prim; PR00189; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
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PROSITE; PS00135; TRYPSIN_SER; 1.

Collagen degradation; Hydrolase; Serine protease; Signal; Zymogen; Glycoprotein.

SIGNAL

PROPEP
29 99 SIMILARITY.

PROPEP
251 254 BY SIMILARITY.

CHAIN 30 250 WYELOBELASIN.

RACT SITE 73 77 CHARGE RELAY SYSTEM (BY SIMILARITY).

RACT SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).

CARROHYD 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).

CARROHYD 170 N-LINKED (GLONAC. . ) (POTENTIAL).

CARROHYD 176 176 N-LINKED (GLONAC. . ) (POTENTIAL).
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Shimohigashi Y., Fukumaki Y., Niwa M., Yamashina I., Hattori S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Accelerated evolution of crotalinae snake venom gland serine
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S -> A (IN REF. 2).
W, 00CEB989A3CB79CA CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Venom serine proteinase 3 precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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MEDLINE=97096898; PubMed=8941719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 AA; 27626 MW;
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Best Local Similarity 66.7
Matches 6; Conservative
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013063;
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SP3_TRIGA
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060259; Q9HCB3; Q9UIL9; Q9UQ47;
15-UUL-1999 (Rel. 38, Last sequence update)
15-ML-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (MP) (Kallikrein 8) (Ovasin) (Serine protease TADG-14) (Tumor-associated differentially expressed gene-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning of tumor-associated differentially expressed gene-14, a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yoshida S., Taniguchi M., Hirata A., Shiosaka S.;
"Sequence analysis and expression of human neuropsin cDNA and gene.";
Gene 213:9-16(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazwa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                         VENOM SERINE PROTEINASE 3.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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SMART; SMO0020; Tryp SPC; 1.

FROSITE; PS00134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

PROSITE; Squal: Signification of the state of 
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3160379F61E9F74B CRC64;
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N-LINKED (GLCNAC. . .)
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MEDLINE=98372070; PubMed=9714609;
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154
154
251
258 AA;
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Best Local Similarity
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ACT_SITE
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SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).

A lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Iamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Brower A., Garnes J.,
Andreise T., Trankheim M., Attix C., Amico-Keller G., Coeffield J.,
Andreise T., Trankheim M., Attix C., Amico-Keller G., Coeffield J.,
A Duarte S., Lucas S., Barce R., Tromas P., Quan G., Kobayashi A.,
A rellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Carrano A.V.;
I "Sequence analysis of chromosome 19413.4.";
C. "Sequence analysis of chromosome 19413.4.";
L. buntted (OCT-2000) to the EMBJ/Genbank/DDBJ databases.
C. "PUNCTION: Suggested to be involved in kindling epileptogenesis and hippocampal plasticity.
C. "CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
C. "CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
C. "SUBCELLULAR LOCATION: Secreted.
C. "Bront-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISOId-060259-2; Sequence=VSP_005401;
-!- TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in the pancreas while isoform 2 is expressed in adult brain and hippocampus. Both forms are alofound in fetal brain and placenta. Not detected in kidney, spleen, liver and lung.
-!- SIMILARITY: Belongs to peptidase family 51. Kallikrein subfamily.
                                                                            SEQUENCE FROM N.A. (ISOFORM 1).

Gan L., Gelinas R., Gown A.M., Moss P., Smith R., Wang K.;

Molecular cloning and characterization of a novel serine protease,

ovasin, a potential molecular marker for ovarian carcinomas.";

Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=205100930; PubMed=11054574;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paeper B., Wang K.;
"Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region.";
Gene 257:119-130(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM, 605644, -
GO; GO:0008236, F:serine-type peptidase activity; TAS.
GO; GO:0007399; P:neurogenesis; TAS.
serine protease overexpressed by ovarian carcinoma."; Cancer Res. 59:4435-4439(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=O60259-1; Sequence=Displayed;
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InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
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EMBL; AF095743; AAD29574.1;
EMBL; AF243527; AAG33361.1;
EMBL; AC011473; AAG3254.1;
HSSP; Q61955; 1NPM.
MEROPS; S01.244;
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EMBL, AB012761; BAA28676.1; --
EMBL, AB010780; BAA88684.1; --
EMBL, AB008390; BAA82665.1; --
EMBL, AB008927; BAA82666.1; --
EMBL, AP055982; AAD56050.1; --
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MIM; 605644; -
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                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.

N-LINKED (GLCNAC. ..) (POTENTIAL)

A -> AACGELDLITTRIYABNIPCVHINPQWPSQPSHCPRG

MSNPLPPAA (in isoform 2).

FP439E5BBC83E660 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93363642; PubMed=7689340; MEDLINE=93363642; PubMed=7689340; Gauthiter Er., Chapdelaine P., Tremblay R.R., Dube J.Y.; Gauthiter Er. Characterization of thesus monkey prostate specific antigen cDNA."; Elochim. Biophys. Acta 1174:207-210(1993).

-I- FUNCTION: PSA presumably hydrolyzes the high molecular mass seminal vesicle protein thus leading to the liquefaction of the seminal coaqulum. PSA is a glandular kallikrein.

-I- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-1-Xaa.

-I- CATALYTIC Belongs to peptidase family SI. Kallikrein subfamily.
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(BY SIMILARITY).
(BY SIMILARITY).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarthini, Cercopithecidae,
Cercopithecines, Macaca.
PROSTIE; PSCOLOGA, TRYPEIN DOM; 1.

DR PROSTIE; PSCOLOGA; TRYPEIN DOM; 1.

DR PROSTIE; PSCOLOGA; TRYPEIN DOM; 1.

PROSTIE; PSCOLOGA; TRYPEIN DOM; 1.

RW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal; RW Alternative splicing.

PT SIGNAL

FT SIGNAL

FT GHAIN

"T ACT SITE 120 120 CHARGE RELAY SYSTEM

ACT SITE 120 120 CHARGE RELAY SYSTEM

ACT SITE 120 120 CHARGE RELAY SYSTEM

ACT SITE 2 2 173 BY SIMILARITY

"T STLFID 39 173 BY SIMILARITY

"T SILE 126 128 BY ST"

"T SIN 186 BY ST"
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01-FEB-1994 (Rel. 28, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Prostate specific antigen precursor (EC 3.4.21.35) (FSA) (Gamma-seminoprotein) (Kallikrein 3).
KLK3 OR APS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 AA; 28048 MW;
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MEROPS; S01.162; -.
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KLK3 MACMU
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(9Y337; OSHBG8;
16-OCT-2001 (Rel. 40, Last sequence update)
15-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Kallikrein 5 precursor (BC 3.4.21.-) (Stratum corneum tryptic enzyme)
(Kallikrein-like protein 2) (KLK-L2).
KAKS OR SCTE.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                  PROSTATE SPECIFIC ANTIGEN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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BY SIMILARITY.
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N-LINKED (GLCMAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brattsand M., Egelrud T.; "Purification, molecular cloning, and expression of a human stratum corneum trypsin-like serine protease with possible function in
                                                                                                                                       Hydrolase; Serine protease; Glycoprotein; Antigen; Zymogen; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINES-20118155, PubMed=10652563;

Yousef G.M., Luo L.-Y., Diamandis E.P.;

"Identification of novel human kallikrein-like genes on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20510030; PubMed=11054574; Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paeper B., Wang K.; Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."; Gene 257:119-130(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 1; Length 261;
Pred. No. 3.9;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                            8525B14B15967E5C CRC64;
                                                                                                                                                                      ACTIVATION PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  desquamation.";
J. Biol. Chem. 274:30033-30040(1999).
InterPro; IPR001354; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfan; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19q13.3-q13.4.";
Anticancer Res, 19:2843-2852(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Stratum corneum;
MEDLINE=99445563; PubMed=10514489;
                                                                                                                                                                                                                                                                                                                                                              28816 MW;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                          65
120
213
173
66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 GPLVCDGVL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GPLVCRGTL 9
                                                                                                                                                                                                                                                                                                                                                            261 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. TISSUE=Ovary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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CHAIN
ACT SITE
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DISULFID
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                                                                                                                                                        SIGNAL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatica Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
BY SIMILARITY.
N-LINED (GLCNAC. ...) (POTENTIAL).
N-LINED (GLCNAC. ...) (POTENTIAL).
N-LINED (GLCNAC. ...) (POTENTIAL).
MISSING (IN REF. 3).
MISSING (IN REF. 3).
MY D92C92F5609E5946 CRC64;
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(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 605643; -. C:extracellular space; TAS. GO; 60:0004515; C:extracellular space; TAS. GO; GO:0004525; F:serine-type endopeptidase activity; NAS. GO; GO:0008549; P:sepidermal differentiation; TAS. GO; GO:0006508; P:proteolysis and peptidolysis; NAS. InterPro; IPR009003; Cys Ser trypsin. InterPro; IPR001254; Peptidase_S1. InterPro; IPR001254; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; irrunia...

Pran, PR00089; trypsin; 1.

PRINT; PR00022; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS50034; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN SER; 1.

Hydrolase; Serine protease; Glycoprotein; Signal.
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CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
CHARGE RELAY SYSTEM (
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EMBL; AF136028; AAD26429.1; -..
EMBL; AF243527; AAG33358.1; -..
EMBL; BC008036; AAH08036.1; -..
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231
231
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173
258
N-
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N-
250
32020 MW
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173
208
252
253
293 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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ó Query Match
76.0%; Score 38; DB 1; Length 293;
Best Local Similarity 66.7%; Pred. No. 4.4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps

1 GPLVCRGTL 9 ||:|| |:| 247 GPVVCNGSL 255

arch completed: March 1, 2004, 17:30:00
b time : 7 secs

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March 1, 2004, 17:20:41; Search time 30.3333 Seconds (without alignments) 93.615 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                    1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                 otal number of hits satisfying chosen parameters:
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Maximum Match 1008
Listing first 45 summaries
                                                                M protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_unclassified:*
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sp_bacteria:*
sp_fungi:*
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50
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sp rodent:*
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erfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	QBnfv7 homo sapien	Q8n5n9 homo sapien	Q9dbq8 mus musculu	Q9cq78 mus musculu	Q9qyn4 mus musculu	Q9qyn3 m hippostas	Q83wx7 streptomyce	Q8g311 bifidobacte	Q9f828 micromonosp	Q9f830 micromonosp	Q8ncw4 homo sapien	Q9xsn6 sus scrofa	Q8qg86 bothrops in	Q9xac9 streptomyce	Q86tg8 homo sapien	Q8keh3 chlorobium
SUMMARIES	QI	Q8NFV7	6NSN8O	Q9DBQ8	090078	Q9QYN4	O9QYN3	Q83WX7	Q8G3L1	Q9F828	Q9F830	QBNCW4	9NSX6Ö	985080	Q9XAC9	Q86TG8	Q8KEH3
	DB	4.	4	11	11	11	11	N	16	N	N	4.	9	13	16	4	16
	Query Match Length DB	181	253	251	87	249	276	612	621	3201	3546	220	254	257	262	286	619
de	Query Match	100.0	100.0	90.0	82.0	82.0	82.0	82.0	82.0	82.0	82.0	80.0	80.0	80.0	80.0	80.0	80.0
	Score	50	50	45	47	41	41	41	41	41	41	40	40	40	40	40	40
	esult No.	-	N	m	4	ß	φ	7	80	σ	10	11.	12	13	14	15	16

Q9ybc2 aeropyrum p	Q9w7q5 paralichthy	Q9nr68 homo sapien	Q9r048 mus musculu	795076 mus muscalu	Q8n4e0 homo sapien	Q86vj5 homo sapien	Q91ve3 mus musculu	Q8wzb4 homo sapien	Q8k597 rattus norv	Q8cgr4 mus musculu	Q8iw69 homo sapien	Q8iu55 homo sapien	Q8cgr6 mus musculu	OSppw7 xanthomonas	Q8p4ul xanthomonas	Q9cs05 mus musculu	Ospbbe was mascala	Q86yz7 homo sapien	Q7x7n0 oryza sativ	Q86yz8 homo sapien	O80xd5 mus musculu	Q8k002 mus musculu	Q8wx98 homo sapien	mus	Q62540 mus spretus	mus	Q9d974 mus musculu	Q9puf3 bothrops ja
Q9YBC2	Q9W7Q5	Q9NR68	Q9R048	Q9CV76	Q8N4E0	Q86VJ5	Q91VE3	Q8WZB4	Q8K597	Q8CGR4	Q8IW69	<b>Q8IU55</b>	QBCGR6	Q8PPW7	Q8P4U1	Q9CS05	QBBPP6	Q86YZ7	Q7X7NO	086YZ8	Q80XD5	Q8K002	Q8WX98	QBCHD0	Q62540	09CVU2	Q9D974	Q9PUF3
17	13	4	I	H	4	4	금	4	금	11	4	4,	11	79	16	Ξ	H	4	10	マ	11	Π	4	11	1	11	11	13
155	247	119	234	234	235	243	249	253	254	254	260	269	276	306	306	514	1180	1235	1246	1260	1301	1310	1311	1481	46	108	114	117
78.0	78.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0			76.0	_		74.0		-	74.0
39	3	38	38	38	38	38	38	38	38	38	38	38	38	38	38	89 13	38	38	38	38	38	38	38	38	37	37	37	37
17	81	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	. 36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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RESULT 1

OGNEYOT PRELIMINARY; FRT; 181 AA.

DA GANEVOT

DA COCT-2002 (TrEMBLrel. 22, Last annotation update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE MAILKrein 7 short variant priotein.

SALIKrein 7 short variant priotein.

SALIKrein 8 Human Nelland Primates; Catarrhini; Hominidae; Homo.

CE Enkaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

CO Manmalis; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CO MAILT TAXID-9606;

RN [1]

RA SAUGENCE FROM N.A.

RA "Human Kellikrein 7 (KLK7) short variant mRNA from ovarian

RT "Human Kellikrein 7 (KLK7) short variant mRNA from ovarian

RT "Human Kellikrein 7 (KLK7) short variant mRNA from ovarian

RT "Human Kellikrein 7 (KLK7) short variant mRNA from ovarian

RT "Submitted (Aud-2001) to the EMBL/GenBank/DDBJ databases.

CH STAILARITY: BELONGS TO PEPTIDASE FAMILY SI.

DR GO, GO:000423; F:PEPTIDASE FAMILY SI.

DR GO, GO:000423; F:PEPTIDASE and peptidolysis; IEA.

DR GO, GO:000423; F:PEPTIDASE and peptidolysis; IEA.

DR GO, GO:000423; F:PEPTIDASE SI.

DR GO, GO:000423; F:PEPTIDASE SI.

DR FARMY: SMOOD20; TYPP-SET.

DR FARMY: SMOOD20; TYPP-SET.

DR FARMY: SMOOD20; TYPP-SET.

DR FARMY: SMOOD20; TYPP-SET.

DR FRANCIS: PROOJ34; PEPTIDASE.

SCOURNE ISLAMS: 10008; Second SI.

Hydrolase; Protease; Serine protease.

SCOURSE ISLAMSE; SCOURS: Serine protease.

SECURNO MATCHES SOURS: SERINE PROCESS.

OLDORY MATCHES 9; CONSERVATIVE 09008; SECURNO SI.

Best Local Similarity 10008; Second O: O:099; Mismatches 9; Conservative 0; Mismatches 0; Indels 0; Gaps
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Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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STRAIN=CSTRL/6J; TISSUE=Lung;
MEDLINE=2108566.0; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Wakaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NGBI_TaxID=10090;
                                                                                                                                                                                                                                                                                             01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Kallikrein 7 (chymotryptic, stratum corneum).
Fuhmo sapiens (Human).
Fukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Straubberg R.,
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
SINULARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBL; BC032005, AAH32005.1; -.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006503; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser trypsin.
R TherPro; IPR001264; Peptidase SI.
InterPro; IPR00114; Peptidase SI.
InterPro; IPR00114; Peptidase SI.
InterPro; IPR00114; Peptidase SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 50; DB 4; Length 253; 100.0%; Pred. No. 0.12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROMINES PROCOSS; CHYDEAN; I.
PRINKES; PROCOZZ; CHYMOTRYPSIN.
SWART; SWOOJZO; TRYPESIN.
PROSITE; PSSOURG; TRYPESIN DOM; I.
PROSITE; PSOULJS; TRYPESIN HIS; I.
PROSITE; PSOULJS; TRYPESIN HIS; I.
PROSITE; PSOULJS; TRYPESIN ERF; I.
PHYGROLASE; PROCEASE; SETIME PICTERSE.
SEQUENCE 253 AA; 27608 MM; 2D68B6A41B22A668 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                         135 GPLVCRGTL 143
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                                   1 GPLVCRGTL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Skin;
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Q8N5N9;
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                                                                                                                                                                                   ESULT 2
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RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Stakai K., Okido T., Furunuo M., Aono H., Baldarella R., Barsh G., RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., RA Greinici S., Hill D., Hefmann M., Hume D.A., Kamiya M., Tee N.H., RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., R. Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamiya N., Storch K.-F., RA Savaki H., Sato K., Storch K.H., Weitz C., Whittaker C., Wilming L., Rymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., R. Hayashizaki Y., Rhuctional annotation of a full-length mouse cDNA collection."; R. Nature 409:685-690[200].

R. Matsuki H., Monder D., Ringwald M., Rodriguez C., Whittaker C., Wilming L., R. Rasalinaki Y., Rawaji H., Kohtsuki S., R. Hayashizaki Y., L., Embl. Akod4807; Ballongs TO PEPTIDASE FAMILY SI.

C. -! SIMILARITY: Ballongs TO PEPTIDASE FAMILY SI.

DR HSSP: PONCES: Judoc. 11.
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KAWAI U., Shinadawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

KAWAI U., Shinadawa A., Shibata K., Konno H., Adachi J., Fukuda S.,

Alawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

B. Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Kochiwa H.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesolo G., Quackenbush J.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesolo G., Quackenbush J.,

Schriml L.M., Staubii F., Suzuki R., Bansh G.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninda M., Genomato M.,

Brownstein M.J., Bult C. C., Fletcher C., Fujita M., Geniboldi M.,

Rushincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Pred. No. 1.1;
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MGD, MGT.1921082; Echymotrypsin activity; IEA.
GG) GO.0004233; F:chymotrypsin activity; IEA.
GG) GO.0004235; F:chymotrypsin activity; IEA.
GG) GO.0004295; F:trypsin activity; IEA.
GG) GO.0005208; P:proteclysis and peptidolysis; IEA.
InterPro; IPRO0903; Cys Ser trypsin.
InterPro; IPRO01314; Peptidase_S1.
InterPro; IPRO01314; Peptidase_S1.
InterPro; IPRO01314; Peptidase_S1.
InterPro; IPRO01314; Peptidase_S1.
INTERPRO; IPRO01314; Peptidase_S1A.
INTERPRO; IPRO0134; IPROFIN.
IPROSITE; PSO0134; IPROFIN.
IPROFINES IPROFIN.
IPROFINES IPROFINES
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01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-UTN-2003 (TrEMBLrel. 25, Last annotation update)
2310015108Rik protein (Fragment).
PRSS20 OR 2310015108RK.
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88.9%; Pred. No. 1...
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Gaps
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PMSSS20.
Mus musculus (Mouse).
Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia; Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
Mitsui S., Yamagushi N.;
Mitsui S., Yamagushi N.;
"CDNA cloning of a novel brain serine protease, Hippostasin.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB016226; BAA88825.1; -.
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                             ;
0
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Pred. No. 2.4;
1; Mismatches 1; Indels
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TISSUBEBRAIN,
Yamaguchi N., Mitsui S.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F9FF9CB457D727D5 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                   249 AA.
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GO; GO:0005576; C:extracellular; IDA.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
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PRINTS; PR07022; CTWMOTRPEIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
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Best Local Similarity 77.8
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SEQUENCE
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Length 249;

DB 11;

Score 41;

82.0%;

Query Match

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SEQUENCE FROM N.A.

C STRAIN-C77BL/60; TISSUE=Tongue;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Anagaki T., Hara A., Hayatsu N., Hiranka T., Hori F.,
Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojina Y., Konno H., Kodda M., Koya S., Kurihara C.,
Antsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Antsuyama T., Miyazaki A., Nishi K., Naito R., Sakai C.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Takahashi F., Tanaka T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Tijma Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBU databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [4]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
THE PANTOM CONSOLTIUM.
THE RIKEN Genome Exploration Research Group Phase I & II Team;
HAP RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length consol."
                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 25, Last annotation update)
Hipportasin prostate type (Adult male tongue cDNA, RIKEN full-length enriched library, clone:2310015108 product:protease, serine, 20, full insert sequence) (Adult male tongue cDNA, RIKEN full-length enriched library, clone:2310040F07 product:protease, serine, 20, full insert sequence)
                    Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CS7BL/61, TISSUE=Tongue;
RIKEN FANTOM CONTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
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MEDLINE=20525466; PubMed=11072088;
Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N.;
Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N.;
hipbostasin/TLSP (PRSS20).";
Biochim. Biophys. Acta 1494:206-210(2000).
                      Indels
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Yamaguchi N., Mitsui S.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=9279253; Pubmed=10349636;
Carninci P., Hayashizaki Y., "High-efficiency full-length cDNA cloning.";
  77.8%; Pred. No. 6.5; ive 1; Mismatches
                                                                                                                                                                                             276 AA
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Local Similarity 77.8
nes 7; Conservative
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                                                                                                204 GPLVCNGSL 212
                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
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                                                             1 GPLVCRGTL
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      Best Loc
Matches
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Q9QYN3
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Mol. Microbiol. 0:0-0(2003).
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                                            SECUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=Tongue;
STRAIN-C57BL/6J; TISSUE=Tongue;
MEDLINE=20499374; Pubmed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and Subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SITAIN=C37BL/6J; TISSUE=Tongue;

STAIN=C37BL/6J; TISSUE=Tongue;

Shibata K., Tech M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

A MEDLINE=2030913; PubMed=11076861;

A Sumi N., Ishili Y., Nakamura S., Hazama M., Nishine T., Harada A.,

A Sumi N., Ishili Y., Nakamura S., Hazama M., Nishine T., Harada A.,

A Yonedo Y., Ishikawa T., Ozawa Y., Izawa M., Ohara E., Watshiki M.,

A Yonedo Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Cazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashiki Y.,

RIKEN integrated sequence analysis (RISA) system-384 format

Genome Res. 10:1757-1771(2000).

C -1- SIMILARITY: BELONOS TO PEPTIDASE FAMILY SI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mochizuki S., Hiratsu K., Suwa M., Ishii T., Sugino F., Yamada K.,
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-GOT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Streptomyces rochel (Streptomyces parvullus).
Plasmid pilolocteria, Actinobacteriaes Actinobacteriaes Streptomycineae; Streptomyceses; Streptomyces.
NCBL TaxID=1928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 11; Length 276;
Pred. No. 7.2;
1; Mismatches 1; Indels
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Best Local Similarity 77.8
Matches 7; Conservative
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STRAIN=LOC 2705;

XM MEDINE=229497;

XM PEDINE=229497;

PERINE=LOC 2705;

PERINE=LOC 2705;

Pridmore R.D., Arigoni F.,

Pridmore R.D., Arigoni F.,

Pridmore R.D., Arigoni F.,

Nationi Sequence of Bifidobacterium longum reflects its adaptation of the human gastroinestinal tract.,

Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).

REMBL; AE014808; AAN25531.1;

RO; GO:0016874; F:ligase activity; IEA.

GO; GO:0016874; F:ligase activity; IEA.

GO; GO:0018152; P:metabolism; IEA.

GO; GO:0008152; P:metabolism; IEA.

RO; GO:0008152; P:metabolism; IEA.

RO; GO:0008153; AMP-bind.

DR PROSITE; PS00687; ALDEHYDE GEHYDR GLU; 1.

PROSITE; PS00687; ALDEHYDE DEHYDR GLU; 1.
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MEDLINE20221737; PubMed=10767533;

SUWA M., Sugino H., Sasaoka A., Mori E., Fujii S., Shinkawa H.,

Nimi O., Kinashi H.,

Nimit O., Kinashi H.,
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                                                                                                                                                                                                         Hiratsu K., Mochizuki S., Kinashi H., "Cloning and analysis of the replication origin and the telomeres of the large linear plasmid pSLA2-L in Streptomyces rochei."; Mol. Gen. Genet. 263:1015-1021(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=7434AN4;
MEDLINE=99053144; PubMed=9836424;
Kinashi H., Fujii S., Hatani A., Kurokawa T., Shinkawa H.;
Kinashi H., Fujii S., Hatani A., Kurokawa T., Shinkawa H.;
"Physical mapping of the linear plasmid pSLA2-L and localization of the eryal and acti homologs";
"I homologs";
"A standard acti homologs";
"A
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01-NAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable long-chain-fatty-acid--CoA ligase, long-chain acyl-COA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Bacteria, Actinobacteridae, Bifidobacteriales, Bifidobacteriaceae, Bifidobacterium.
NCBI __TaxID=216816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match B2.0%; Score 41; DB 2; Length 612; Local Similarity 77.8%; Pred: No. 16; 1; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein, Plasmid.
SEQUENCE 612 AA, 66525 MW, 9BF0E1EE8D3110FC CRC64,
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                                                                                       STRAIN=7434AN4;
MEDLINE=20408175; PubMed=10954087;
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SEQUENCE FROM N.A.
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FADD4 OR BL1748.
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Q9F828

RESULT 9

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3546 AA.
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=NRRL3275;
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      DDATATARE REPORTED TO THE PROPERTY OF THE PROP
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Volchegursky Y., Hu Z., Katz L., McDaniel R.;

Volchegursky Y., Hu Z., Katz L., McDaniel R.;

Volchegursky Y., Hu Z., Katz L., McDaniel R.;

Nobsythesals of the anti-parasitic agent megalomicin: transformation of erythromycin to megalomicin in Saccharopolyspora erythraea.";

Mol. Microbiol. 37:752-762(2000)

-!- SIMILANITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

EMBL, AF263245; AAG13919.1; -.

HSSP: P25715; IMLA.
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                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micromonosporineae; Micromonosporaceae; Micromonospora.
NCBI_TaxID=136926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.0%; Score 41; DB 2; Length 3201; 77.8%; Pred. No. 77; 1; Indels 1; Mismatches 1; Indels
                                                                                                 Query Match 82.0%; Score 41; DB 16; Length 621; Best Local Similarity 100.0%; Pred. No. 16; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; Phosphopantetheine; Transferase.
SEQUENCE 3201 AA; 334781 MW; 44BDA30E14855650 CRC64;
          Ligase, Complete proteome.
SEQUENCE 621 AA, 67948 MW; 5BCDDB4B5BF3083A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Megalomicin 6-deoxyerythronolide B synthase 3.
MEGAIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 3201 AA
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; PS00012; PHOSPHOPANTETHEINE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF02801, ketoacyl-synt C, 2. Pfam, PF00550, pp-binding, 2. Pfam, PF00975, Thioesterase, 1.
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Pfam; PF00106; adh_short; 1.
Pfam; PF00109; ketoacyl-synt; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                      1 GPLVCRG 7
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Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micromonosporineae; Micromonosporineae; Micromonosporaceae; Micromonospora.
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SEQUENCE 3546 AA; 371191 MW; 86C6794E95415BBC CRC64;
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01-007-2002 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
prostate specific antigen precursor.
01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Megalomicin 6-deoxyerythronolide B synthase 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SDR) FAMILY.

EMBL, AFCS4245, AG433917.1;

HSSP, P254215; JMLA.

GO; GO:0016491; F:candoreductase activity; IEA.

GO; GO:0016491; F:transferase activity; IEA.

GO; GO:0006401; F:transporter activity; IEA.

GO; GO:0006515; F:transporter activity; IEA.

GO; GO:0006152; F:metabolism; IEA.

GO; GO:0006152; P:metabolism; IEA.

InterPro; IFR00127; Actrans.

InterPro; IFR00129; Actrans.

InterPro; IFR00129; Actrans.

InterPro; IFR000196; Ada Short.

InterPro; IFR000196; Ada Short.

InterPro; IFR000196; Ada Short.
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TISSUE=Prostate;
Heuze-Vourc'h N., Courty Y.;
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RESULT 10 Q9F830

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Q9XAC9
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warker PSA (prostate-specific-antigen).";

submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

-1. SIMILARITY: BELONGS TO PEPTDAGE FAMILY SI.

EMBL, AJ459782; CDBJ00844.1;

EMBL, AJ459782; CDBJ00844.1;

GO; GO:00004263; F:chymotrypsin activity; IEA.

GO; GO:0004263; F:peptidase activity; IEA.

GO; GO:0004263; F:peptidase activity; IEA.

RO; GO:0006208; F:peptidase SI.

InterPro; IPR001254; Peptidase SI.

InterPro; IPR001254; Peptidase SI.

InterPro; IPR001254; Peptidase SIA.

PRINTS; PR00722; CHYMOTRYBIN.

PRNSTIE; PS00202; Trypsin; 1.

PRNSTIE; PS00125; TRYPSIN DOM; 1.

PROSITE; PS00135; TRYPSIN LHIS; 1.

POTENTIAL.

PROSITE; PS00135; TRYPSIN LHIS; 1.

POTENTIAL.

STAMAL SUMMAL SECTIONAL SECT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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OLINOV-1999 (TrEMBLrel. 12, Last sequence update)
OLINOV-1999 (TrEMBLrel. 12, Last sequence update)
OLIOCT-2003 (TrEMBLrel. 25, Last annotation update)
Enamel matrix serine proteinase 1 precursor.
Enamel matrix serine proteinase 1 precursor.
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria, Cetartiodactyla, Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 POTENTIAL.
254 ENAMEL MATRIX SERINE PROTEINASE 1.
27235 MW; FD40EF85664406F1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.0%; Score 40; DB 4; Length 220; 77.8%; Pred, No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aydrolase, Protease, Serine protease, Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 77.0
77. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GPLVCRGTL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 AA;
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SEQUENCE
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An Unqueira de-Azevedo I.L.M., Ho P.L.;

Unqueira de-Azevedo I.L.M., Ho P.L.;

Unqueira de-Azevedo I.L.M., Ho P.L.;

pitviper Bothrops insularis through the generation of Expressed

RT pitviper Bothrops insularis through the generation of Expressed

RT pitviper Bothrops insularis through the generation of Expressed

RT Sequence Tags (ERTS) ";

REMBL; AF490354; AM009635.1; ---

REMBL; AF490355; Fichymotrypsin activity; IEA.

GO; GO:0004233; Fichymotrypsin activity; IEA.

GO; GO:0004235; Fichymotrypsin activity; IEA.

GO; GO:0004235; Fitrypsin activity; IEA.

GO; GO:0004235; Fitrypsin activity; IEA.

RC; GO:0004235; Fitrypsin; I.

RC; GO:0004235; Fitrypsin; I.

RC; GO:0004235; Fitrypsin; I.

RC; GO:004236; Fitrypsin; I.

RC; GO:00423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Serine proteinase
Bothrops insularis (Island jararaca) (Queimada jararaca).
Bothropta: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
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Streptomyces coelicolor.
Streptomycineae, Streptomycetaceae, Streptomyces.

MCBLTaxID=1902;
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Best Local Similarity 75.0%; Pred. No. 10; Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 1; Indels
Score 40; DB 6; Length 254; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 24, Last annotation update)
Putative aminoglycoside acetyltransferase.
SC01927 OR SCC22.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 AA.
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                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
    Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                              209 GPLICNGSL 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=A3(2) / M145;
STRAIN=A3(2) / M145;
MEDLINE=21996410; FubMed=12000953;
MEDLINE=21996410; FubMed=12000953;
MEDLINE=21996410; FubMed=12000953;
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0016991; F:gentamicin 3'-N-acetyltransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR003679; Antibiotic NAT.
InterPro; IPR003679; Antibiotic NAT.
Transferase; Complete proteome.
SEQUENCE 262 AA; 27930 MW; 0D239D41795A0B93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."; Nature 417:141-147(2002).
BMB1, A19999110; CABE0752.1; -...
PIR; T35999; T35999.
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80.0%; Score 40; DB 16; Length 262;
Best Local Similarity 88.9%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                          STRAIN=A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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TISSUB=Peripheral Nervous System;
Strausberg R.;
Submitted (SPR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC050595; AAH50595.1; -
GO; GO:0004263; F:chymetrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
InterPro; IPR009003; Cys_Ser_trypsin.
  STRAIN=A3(2);
Seeger K., Harris D.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q867G8;
01.JUN-2003 (TrEMBLrel. 24, Created)
01.JUN-2003 (TrEMBLrel. 24, Last sequence update)
01.OCT-2003 (TrEMBLrel. 25, Last annotation update)
Kallikrein 3, (Prostate specific antigen) (Fragment)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 AA.
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                                                                                        [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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DR InterPro; IPR001254; Peptidase_S1.

DR PRINTS; PR0001314; Peptidase_S1A.

DR PRINTS; PR0001314; Peptidase_S1A.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PROSITE; PS000134; TRYPSIN_DOX; 1.

DR PROSITE; PS000134; TRYPSIN_HIS; 1.

DR PROSITE; PS000135; TRYPSIN_HIS; 1.

SQ SEQUENCE 286 AA; 31665 MW; 711E2ECE3ACE4FED CRC64;

Query Match

Author 10 PhVCRGTL 9

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Db 240 GFLVCNGVL 248

Search completed: Match 1, 2004, 17:34:52

Job time: 32.3333 secs
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